



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/1673,605
Source: PCT 09
Date Processed by STIC: 2-27-2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
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Does Not Comply
Corrected Diskette Needed

See page 10



PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/673,605

DATE: 02/27/2002
TIME: 13:33:36

Input Set : A:\Ep.txt
Output Set: N:\CRF3\02272002\I673605.raw

4 <110> APPLICANT: The President and Fellows of Harvard College
6 <120> TITLE OF INVENTION: REGULATION OF BIOFILM FORMATION
9 <130> FILE REFERENCE: 00246/505WO3
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/673,605
C--> 11 <141> CURRENT FILING DATE: 2000-10-17
11 <150> PRIOR APPLICATION NUMBER: 60/102,870
12 <151> PRIOR FILING DATE: 1998-10-02
14 <150> PRIOR APPLICATION NUMBER: 60/083,259
15 <151> PRIOR FILING DATE: 1998-04-27
17 <160> NUMBER OF SEQ ID NOS: 49
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

ERRORED SEQUENCES

21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1090
23 <212> TYPE: DNA
24 <213> ORGANISM: Psuedomonas fluorescens
26 <220> FEATURE:
27 <221> NAME/KEY: variation
28 <222> LOCATION: (1)...(1090)
29 <223> OTHER INFORMATION: n is a, t, c, or g.
31 <400> SEQUENCE: 1

E--> 32 gagcgcagna gaggaagngn gggagganga ggaaggagga gagnggaaga agggggggaa
W--> 33 60gggaggggg aagggagagn ggggagnng gggnatnngg gannngggng gggngnggn
W--> 34 120ntgnttatna tnangctccg gccggacgaa gaaattcccc atgcatttgct cgagcgcgt
W--> 35 180ggcctgtctc gggacaaggta caaccacgta tttagcaaa tgctcnagggc ggaantgctg
W--> 36 240ctgcgcgaac tggcctcgca nttagccac ggctgaatag gctcgcccg tcattttgatc
W--> 37 300tttcccacgc tctgcgtggg aatgcataccc gtgacgctct gcgtcacatc tcagaagcg
W--> 38 360aacgcggagc gtcctggcg acnttcccnc ncagggagcg tggggaaaccn ancaaacntg
W--> 39 420gtccctcga ttntaaaggta cttccttaaa ancttcttnc gggcttccag ggtattttgg
W--> 40 480tccanccccc ttgggaaccc anatccccca ggcggcccg ggttgccccn tttgatcctg
W--> 41 540gggattccga ctttgttccct tgnaaatccc cccttccatt gaaaccnccc angtttngcc
W--> 42 600ttttgttcc ctttggggcc ntnccatcc gntngggcaa aaacgccccat tanggggcng
W--> 43 660gggcggtccc ccccccncg nntgttactn aantncanaa cgccnnnttgg gccanaaaann
W--> 44 720tcgnctngng nnnnnncnnc gncntcttn ctncccntcc nnctntnnt cctcngtgt
W--> 45 780tntccaantc ntnccnncgc ccntccngcc tccccactnc ctnngccctc cnnnccnnnc
W--> 46 840cgtnccatn ctccncntn ntccgcttnt ccccnnnttan cgtngccgtt ncccgcccg
W--> 47 900nnccnnngtca tcnntgncgc tcttccnccc ncctgtccn cccantgccc ngnnnctccg
W--> 48 960aggtegcngg tctcncncc nccngnttcg tgcnccngcn cnngatccc ttcncnccng
W--> 49 1020nccntnatgc tgaccagttn gngngngtng nnccctccc tcngnacntg tntngngggg
E--> 50 1080gggccccccc

Numbering of nucleotide
sequence must be to the
right of each line. See
37 CFR 1.822 (c)(1)-(7). Also,
see sample provided
at back

1090

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Input Set : A:\Ep.txt

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52 <210> SEQ ID NO: 2
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 54 <212> TYPE: DNA
 55 <213> ORGANISM: Psuedomonas fluorescens
 57 <220> FEATURE:
 58 <221> NAME/KEY: variation
 59 <222> LOCATION: (1)...(277)
 60 <223> OTHER INFORMATION: n is a, t, c, or g.
 62 <400> SEQUENCE: 2

E--> 63 ggnnggggnng ggncttgtgtataaaatntca ggctctgaca tccaggccgc aggcggcctg
 W--> 64 60gtccccnatgg ttatcgacca ntccgcccgc ggcnaangtg cctatnanat ctactcncgt
 W--> 65 120ctgtcaang aacgcgtcat ctttctggtg ggcccggtaa aagactacat ggccnacctg
 W--> 66 180atctgtgcgc aactnttggc cttgaanc naaaaccgn acnaggatata ccatcttat
 E--> 67 240atcaacnccc cnggtacttag ttcaaccgt gaaaaaaa 277

69 <210> SEQ ID NO: 3
 70 <211> LENGTH: 819
 71 <212> TYPE: DNA
 72 <213> ORGANISM: Psuedomonas fluorescens
 74 <220> FEATURE:
 75 <221> NAME/KEY: variation
 76 <222> LOCATION: (1)...(819)
 77 <223> OTHER INFORMATION: n is a, t, c, or g.
 79 <400> SEQUENCE: 3

E--> 80 gctngtgtct acgcntcagc aanaatgccg cccgcgacna caacncttaa tcngtga
 W--> 81 60ntccattgga tgatgtccca cccgtccatc cnancctgga agccaggatt nctgcccac
 W--> 82 120atnanggtnc gggtggcaac aatctcaccg naacctgnnc ctgtggtcac aancgagg
 W--> 83 180caggtcacca cggncgtccc ggcacccgtt gcccnctgg tcagggcggg ccagggnncg
 W--> 84 240gtngcccaag angtnatcc tcccttgac cctnaancng accgcncna tgcntggcna
 W--> 85 300ccnttgcntt tggcaatgga ccngggngga catnttnccg cccgtatcc agggcncnac
 W--> 86 360ccaanantac ngccccggcg tccctctann ntntactatt cnacgcgtgg gcananntgc
 W--> 87 420ccctngtngg cttnccttcc ttttccccgn cnccntttt tcccnnnntt tttttgnnc
 W--> 88 480gncccncctc cnntccctnc cttccnccnnn cnctcgtctn nnncctngt ggccctcncc
 W--> 89 540cccttntct tccttcnccn tttnctccg tgccctnct ctctgnttcc ncncngtngc
 W--> 90 600gtccgggtan cccagcctcg ctctccnccg ctgnngcnct ctntttctt gttcncntt
 W--> 91 660ccctgtggcc ctntgcgtac ncncnanctt ctccctcgtctn nggtcncanc cttcngtntc
 W--> 92 720cgcnngngnc gnccnccctnc tctngcnccn nnntcgtctt cgtnnnccnng tnctnnnnnc
 E--> 93 780ncagtcnngt gtngnnagnt tnncgnagtn tgnnatccc 819

95 <210> SEQ ID NO: 4
 96 <211> LENGTH: 832
 97 <212> TYPE: DNA
 98 <213> ORGANISM: Psuedomonas fluorescens
 100 <220> FEATURE:
 101 <221> NAME/KEY: variation
 102 <222> LOCATION: (1)...(832)
 103 <223> OTHER INFORMATION: n is a, t, c, or g.
 105 <400> SEQUENCE: 4

E--> 106 gatggtatcg gtnactcggt caccgctggg gtgggtctcg gaacaggatcc tcgaagttcc
 W--> 107 60cgccagtgcc cttatcgatg ctgacttcaa ctttgcggcgc gtctttgttag acgtcgatctt
 W--> 108 120ttgggtgcgtc gacagtcacg gtggcgccgc agcgatgtt atcaccgcgc

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W--> 109 180cgttgctca ggtcacagtg acaggcgc acgcggcg ttgtcaagg ttgtcaagg ttgtcaagg
 W--> 110 240cgatcgaa acc gcctccgca acgctatcg ttgcactcaa agtcaggccg gtatgtcct
 W--> 111 300gaatgtctgt nanngtgggt tcngccggg tggcgccan gtccaatatt tcataatnc
 W--> 112 360naccntgggg tcctccan ntannctaa gttatcgccc ccccccaag gtccttng
 W--> 113 420cgtnacnaaa ttccaccgann ccganctggc nccnaaccgg aangtgang gtctggccg
 W--> 114 480ttcnacang gttnnataac caaacggAAC ntcgggtcac eggttcntt taacngaagg
 W--> 115 540nggtgttna accncggncncc nnctccgg ccaangngng aaattnncng gtggnggaa
 W--> 116 600aanaggtcna ngttttnaan gggttccng tnancntcnt nnncccnan ggnnttnttn
 W--> 117 660ntnanaaaacc aaanntcncc ngaatttncc nccnggtngg nttnncng nannnngaa
 W--> 118 720nttnnnnggt gggnnnnccn ntccttgc tttnaaaatna nncnnttng ggnccnnnc
 E--> 119 780naaaaagggnnc annngnggnnc nnntgggnn ggnncnnn ggnccnaag nt 832
 121 <210> SEQ ID NO: 5
 122 <211> LENGTH: 1054
 123 <212> TYPE: DNA
 124 <213> ORGANISM: Psuedomonas fluorescens
 126 <220> FEATURE:
 127 <221> NAME/KEY: variation
 128 <222> LOCATION: (1)...(1054)
 129 <223> OTHER INFORMATION: n is a, t, c, or g.
 131 <400> SEQUENCE: 5
 E--> 132 cncaanggcn cagagcacag gatatgcngc aatctcatgg acaaacggcg ccagccnat
 W--> 133 60ggaggccacc gacnccacat ccgtcgccg ggtcgcttc aggcncgcca acgcancctc
 W--> 134 120aagggtctgc gccanttgc ncncnccctc gcncaccanc nnagttgcc agcncnccaa
 W--> 135 180actccccacc ncnaannncnc nttnacnaat ntgggttgc cgnataccgc ccncactc
 W--> 136 240gcaccaattt ctcacccncg gcctgaacna actggtcggt ncncncccg cccatccnc
 W--> 137 300tggtttnaac nggcnattt cttnacccccc agcaacancn aataaccgg acctggccan
 W--> 138 360cnccgggtng ctcacccggg cattaaactg cattttcaaa atatnnccgg ttggccacgc
 W--> 139 420ccgttaggtt gtcctgttag gatccnaccc ccanttcnc tntggccctn ggnctgntcn
 W--> 140 480nggaangnn ccntgagct tctcgaccat ctgggtttct tnctcntgen cccactcncg
 W--> 141 540nnncaagttt taaggtnnn nctccggna atcctctng gcnannctt naactgnaaa
 W--> 142 600cttccnccga acngggncct aanantagn cttatnnggg nnacngcgt tgnccaaaccn
 W--> 143 660aactntttt tttcccagc cgcgggctn ttcagaatc tgaacgnaac tcctcnngtc
 W--> 144 720nttccacang gnctcccccc tantnttaa ccgcgtntcn tctatnttgg gngtccccgn
 W--> 145 780ntncatacat gnncngagtan aagaagctn ancctccna nnngntctc cggccccc
 W--> 146 840tttntccctt ctctccctt nancntctaa atatattctt tnntgggnnt naanaagggg
 W--> 147 900ggcgcanaaa nacntntctc cgggggggt tgcgggnctt nnanaaacc cccttctnt
 W--> 148 960tnnnnnccccc ctcacccggg ggctccnccc tccctnttgc tttcccncc ctannaatcc
 E--> 149 1020ctactcncng gncttagttga aaaaacanna acgc 1054
 151 <210> SEQ ID NO: 6
 152 <211> LENGTH: 880
 153 <212> TYPE: DNA
 154 <213> ORGANISM: Psuedomonas fluorescens
 156 <220> FEATURE:
 157 <221> NAME/KEY: variation
 158 <222> LOCATION: (1)...(880)
 159 <223> OTHER INFORMATION: n is a, t, c, or g.
 161 <400> SEQUENCE: 6
 E--> 162 ncnnacgnnt ngnaagtat caggccnattt aaacnnntga cnaaannnaga acangnnggt
 W--> 163 60ctgttactac tcttcaagac caaccaagn cgaccgtgn a tagcgnccncc tntacgcagc

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W--> 164 120atcngttccn cattagatt nntatccatc cntaagttc nccgggtcag aacgntnctt
 W--> 165 180gacgtacaac ccatanngcg gggtaanngg nnattttng ctacctcnca tgtttgaa
 W--> 166 240gnccnanc ccenttaatng gnagcnnnc ncangcnnn ggggattatt acnactcnac
 W--> 167 300ccntgganaa cnttgcact acngcngnc ccccgcngng tccnggnctc ccctgcccac
 W--> 168 360ttcccttg tccecgncctc tntnccccct ttcnctgtn ncttctggtg tncgnttccc
 W--> 169 420ctccccccng tccctcntca ncnnctngcg tctngggcac ctngncgnnc tcttccctnc
 W--> 170 480tggccctct nncccccnnt cgtnntancc ctctctcnca cntncttcat cccgtccctn
 W--> 171 540ttcttntct cnctnccn ccctntccta ntctntctgt cccnctncgn tnctcgtn
 W--> 172 600cctncnccnc ttntcgactt cnncntgtt nccnccnc gcngncttct ctngtcttct
 W--> 173 660cccgtcngcn gtcagnncc cntccttccn ttnctnctn ctgtccgncn gcgncctgt
 W--> 174 720ncctnecncc cctagnnngg ncgcgcctn gcnncctgt cccnngntnt nntcttctg
 W--> 175 780cnccgtgctc nnnttctn tntcnctcg cccatccnct ncctctn nncgtngntt
 E--> 176 840ccncttctag gnccnnattc cnannncngg ccntncccc 880
 178 <210> SEQ ID NO: 7
 179 <211> LENGTH: 779
 180 <212> TYPE: DNA
 181 <213> ORGANISM: Psuedomonas fluorescens
 183 <220> FEATURE:
 184 <221> NAME/KEY: variation
 185 <222> LOCATION: (1)...(779)
 186 <223> OTHER INFORMATION: n is a, t, c, or g.
 188 <400> SEQUENCE: 7
 E--> 189 ncaanncaga tcctgnaaaa cgggaaagg tccnttcagg tacgctactt gtgtataaaa
 W--> 190 60gtcaggccc aaacgcccc ggtgcaacaa ctggtcnaag gctacntggc gggttacaac
 W--> 191 120cgtgcgctgg tcnacacgcaa ggc当地 aatgtgccag cnaatggta
 W--> 192 180cggccgatca cggcgctgga cctggtaag ttgaccgc ggctgttgg ggaaggggc
 W--> 193 240gtcggccagt tgc当地 cctggccggc ggc当地 accgc cccaggcnac cgc当地 cgc当地
 W--> 194 300ggcacccccc tcacggttt cggccggcc gcaacccggc agcagcnnn tggccctgaaa
 W--> 195 360cgccgcaaca atgc当地 tggg cc当地 cggcan cnaacgctcg tt当地 atggc cgttnggaat
 W--> 196 420nttgc当地 gg caaaccccc attttcccg tt当地 ggtttagg cggcattct tttctnacca
 W--> 197 480naaagcacct gaaccattcc cggcaanct tggaaattct tggcccccng ngcctgcca
 W--> 198 540tttgc当地 aaatcaanat cggttcaac canccncctt gc当地 tggacc aaaccgtcaa
 W--> 199 600aaactccaaa aaaattcccc ct当地 cnctt gcaatcnntc naagaaccaa cc当地 ttttn
 W--> 200 660ccaaggatt ttttccna naaacncaa angtntttnt naatttacn acttaaggcc
 E--> 201 720anttnnaaag tncccaattt tt当地 angtcc aatttgnccc nattttaaag gctccgggtt 779
 203 <210> SEQ ID NO: 8
 204 <211> LENGTH: 848
 205 <212> TYPE: DNA
 206 <213> ORGANISM: Psuedomonas fluorescens
 208 <220> FEATURE:
 209 <221> NAME/KEY: variation
 210 <222> LOCATION: (1)...(848)
 211 <223> OTHER INFORMATION: n is a, t, c, or g.
 213 <400> SEQUENCE: 8
 E--> 214 gcccnnncnc nattatncaa gntctaagt ttnnaccana tnccaaaggac ataatgactt
 W--> 215 60nccttatta antgtccgga ccatnccata tnccaaaggactt canaccgtt aacttacc
 W--> 216 120ncatgnctcc gntgtcgta tt当地 anncc ccataagctt cnccgtcag aacgtncaa
 W--> 217 180taggtacant natactgcnc ggc当地 catggc attttggctt tctttagtgg ngnagtt
 W--> 218 240aacagcctt tt当地 gagcgcc tccacagctt tagggggaaa ntnctattca acnctggcna

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W--> 219 300aantttgaaa aactnaganc ttcnnggtt tatagggta tcccntgacc aaannccnct
W--> 220 360aattccnacn ctttgntccc acttcctccc tngcgcgnct ttacnnngng ccccgtccct
W--> 221 420tccccncnng ncntnggnca cnnggggaaa ngnnntcncc ccgtgggttt ctcccngtn
W--> 222 480tngnnnnnc tcgtgnntcc cggncctt ccccccngtt cggaactntt ctcccctncn
W--> 223 540cccncgcng tgctctnnn tnncnngn tncnenggnt tncnengcen ccntttcctc
W--> 224 600ccccccccc ttanccngga nccctctccc tncgcntggc cngeccccn ggnccctccc
W--> 225 660ctntccctc ggnngncnnc gnncnctcc ttnncnnttc cctctccnn ccntcnntc
W--> 226 720cnctcnnc nntccnnnc ctcntnnntc cccentgccc nnnncnccgg ccnttcgnnc
W--> 227 780ctcnnnnnn tncctngncc cgcgtgcncn gtngcgnccc gctntcctgc ctgtcncccc
E--> 228 840ccctnccc 848

230 <210> SEQ ID NO: 9
231 <211> LENGTH: 533
232 <212> TYPE: DNA
233 <213> ORGANISM: Psuedomonas fluorescens
235 <220> FEATURE:
236 <221> NAME/KEY: variation
237 <222> LOCATION: (1)...(533)
238 <223> OTHER INFORMATION: n is a, t, c, or g.
240 <400> SEQUENCE: 9

E--> 241 tatttgtgtta taagntcagc gccagcagt accgatgtca ccgataccat cgacaccaggc
W--> 242 60accgtttcgc tcacagcgac ttgcacgggtg gccgaagggtg ggactgtcggt ttacaccgccc
W--> 243 120tcggtaacg caccgtgac cgacgctccg ttggttatca ccctgttcca aacggccana
W--> 244 180ccatcnccat tccgggttggn gccagcancn gcaccgtgaa cttcggtgaca ccaaacgacg
W--> 245 240ccctcgccgg cggcgataac ctgagcgtga agattgtatga cgccaagggt ggcaattacn
W--> 246 300aaaaactgga catcgacgccc accccgccgg acaccaccgt taccatntg caggacacta
W--> 247 360ccggccgtgac cttgantgca accgatagcg ttgctgaang cggntcgtatc gtttacaccg
W--> 248 420caacattgac caacgcnncc ggntcgcctg tcnctgttnac cctgaacaac ngngcgggtga
E--> 249 480tcaacatccc tgccccgggt tcccccccg tnctantcta cacngngnaga aaa 533

251 <210> SEQ ID NO: 10
252 <211> LENGTH: 591
253 <212> TYPE: DNA
254 <213> ORGANISM: Psuedomonas fluorescens
256 <220> FEATURE:
257 <221> NAME/KEY: variation
258 <222> LOCATION: (1)...(591)
259 <223> OTHER INFORMATION: n is a, t, c, or g.
261 <400> SEQUENCE: 10

E--> 262 tgatttgtgtta taagatcagc cagcaaggcg ccgtcgccgg gttggtaaag cccaccaggc
W--> 263 60aacttggcca gggaaacttt gcccggccg ctggggccaa ttagtccnat tttctcgccc
W--> 264 120ggcttganca ccaggttnat attctacacc tnnggnttct gctgttcgg anaaatnaaa
W--> 265 180nttcaactna nnngnattcca acggccctt ccagaacttt cnggtcangg ggnngctcncc
W--> 266 240caaattgcgc tcttggggca gctccntcat ctgggtcana ganatcttgg tcacccccc
W--> 267 300ctgttggtat cgggtcncat ngnccnacaa cnaaaccaac nggctgaggg cgcgaccgct
W--> 268 360gaacatntt cangcgacca ncccaaccnt gctcangcna cggcgatna tcaagtnaac
W--> 269 420nccnaaaaana anatgaccac cccngccagt tnctggatca acaaagtat gttcttgc
W--> 270 480nggcccggana acatcttccac ccccaattct aagcggctga aggtgccat agtctgttcc
E--> 271 540cnctggatt ggcgtncncc ccccaattact antcaacncn tggnaaaaaa a 591

273 <210> SEQ ID NO: 11
274 <211> LENGTH: 1249

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275 <212> TYPE: DNA
 276 <213> ORGANISM: Psuedomonas fluorescens
 278 <220> FEATURE:
 279 <221> NAME/KEY: variation
 280 <222> LOCATION: (1)...(1249)
 281 <223> OTHER INFORMATION: n is a, t, c, or g.
 283 <400> SEQUENCE: 11
 E--> 284 ctgggtgtat aagatcaggg ccantngtgt cctggagtgt ctgtacagt ggttcggca
 W--> 285 60ngcttgcctt cnanatncan ttttcgtaa ttgccaccct atggctnct ccnaatttga
 W--> 286 120ancacnagnn acctncccan tgncaagggc ttcttcngcn tcnnngaatt canccnacnn
 W--> 287 180naaatnnggc caaccctgan tggttaccgt cntgcccnc ccnctcnggn catttcttg
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 W--> 295 660ntnnngcgggn cgcnccnctt gtccctcnn aaccctgggg ntngcgagcn tacnggctcn
 W--> 296 720ctccctaata tnctggggcgn tnchnngggcgn naacgtcctcg cttcgttca naaatnntc
 W--> 297 780ntaanttcca acntcgngcn gcccgcctcc ggnnnnnnca atntntctc cccctattc
 W--> 298 840tngctacnca gcgngtgatn atcccnntctt canagccctn ttcngggat aacngngnag
 W--> 299 900nganncttc tcttttagtnc cnnaanccna tctctnctcc tcttcttcng gtcgcgcctnc
 W--> 300 960tanancnctg gtcagttnnm tcctcnatgn nnccnnggnt cccnntntct cnctcnctt
 W--> 301 1020ttgnnnactc ccngtntgtc cnggantgggn tcttccgcct eggnancnnt gctctntnt
 W--> 302 1080tcncannncg aanantctcc ttnctaaca nccttcgccc aanachnttt nactctnccc
 W--> 303 1140tcntccttcn ctnnctcgtc tnattntnan ttncnntnct anncngtgac tcgttagcnc
 E--> 304 1200tccngtctt ccnancnttc gcccncntcc cnccnctnca nnctatccc 1249
 306 <210> SEQ ID NO: 12
 307 <211> LENGTH: 373
 308 <212> TYPE: DNA
 309 <213> ORGANISM: Psuedomonas fluorescens
 311 <220> FEATURE:
 312 <221> NAME/KEY: variation
 313 <222> LOCATION: (1)...(373)
 314 <223> OTHER INFORMATION: n is a, t, c, or g.
 316 <400> SEQUENCE: 12
 E--> 317 tnatttgtta taagnntcagg actagagntc ctcttttagt naacggttcgc agcgaaaa
 W--> 318 60accgcacgtt ccantgcgtt ccccaccccg tactagtgcg cacgtggana aactcgcccc
 W--> 319 120gagtcgacnc gtgggtanta gtcgaagcgt ggnganggnt cncgntatna ggcntaan
 W--> 320 180ctgcacgtt aaagcngggg gaaggttctc naaaanttcn ccnatgaggg agaacacgg
 W--> 321 240aanccctta ccncaggggc ggccngaaa tctggcaacn ganccgnngg agaatacncc
 W--> 322 300atttcgttagt cttccatgggc accaccggga acatcatggg cgtcnnntnc cngtactant
 E--> 323 360cgaccgtggc caa 373
 325 <210> SEQ ID NO: 13
 326 <211> LENGTH: 683
 327 <212> TYPE: DNA
 328 <213> ORGANISM: Psuedomonas fluorescens
 330 <220> FEATURE:

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331 <221> NAME/KEY: variation
 332 <222> LOCATION: (1)...(683)
 333 <223> OTHER INFORMATION: n is a, t, c, or g.
 335 <400> SEQUENCE: 13

E--> 336 tgactgtgt ttataagntc agnccacnt ggnagtcnc ntntgggtgg tangatccgc
 W--> 337 60ancnattaag ctggccnnng gaaanticngg ttcaacccgn tgcnngaat ganncnntat
 W--> 338 120ttcaactcncc cggcgtnac ncctnngtan tantcgaccc ntggncanta ntantctaca
 W--> 339 180nnttggtcaaa acnnttcgan nnngtaggng ncgccttnn tanangtnan cttegttnacg
 W--> 340 240ggggaggaaa angctccccg gnggcannn gccgagccct aaaaangagg cangtanggg
 W--> 341 300tgnngaaaaaa naatanctng atangacncc acccnnttg acgccaatta accgangtac
 W--> 342 360angacccnng cnactcatt ttnagtgtnc gcgacagaaa ttttanggn cgcnccangn
 W--> 343 420gaanggntct cnangttnn gnaaanlnaa acnaggccct ccnnntaaatg gtggaccgc
 W--> 344 480ggnnnaanntt nnccncgant ggggtttga aattacttt caacaatctt caaaacntcc
 W--> 345 540gggtcnanc accgaggggnnc aaaaaaaaaa ntnttccgn gtngccnnna aaatatccna
 W--> 346 600aattttntcn cccccccccc nccnnnaaag aagggnnggg gggaaaggggaa aaaagggggg
 E--> 347 660aangaggggg gggaaagggggg ggg 683

349 <210> SEQ ID NO: 14
 350 <211> LENGTH: 672
 351 <212> TYPE: DNA
 352 <213> ORGANISM: Psuedomonas fluorescens
 354 <220> FEATURE:
 355 <221> NAME/KEY: variation
 356 <222> LOCATION: (1)...(672)
 357 <223> OTHER INFORMATION: n is a, t, c, or g.
 359 <400> SEQUENCE: 14

E--> 360 gtgttgtataagntcag nccctggcct gngcncnac aactccgttn nccgtctaca
 W--> 361 60nttttagcnaa ggatcggtca ttgcctngtc tnctggntan actnccggga cnatccacct
 W--> 362 120caataactccn nccattnacg tctatggtaa cncggaggtc ggtcancagn ncattaccg
 W--> 363 180gtntcacnng tggaaacttc gaaaatctng tggcnaacac gggacctgcg gtcccnccna
 W--> 364 240nttccgattc ngngananacn ncatggntgt cncnnacnng nngcnacncc attcctgnan
 W--> 365 300gggnccaan ttcctttcnc ntcaanccgt ngnnaacggg cccnaatncc gttaacggtt
 W--> 366 360ccnnngananaa atggtcngtt ttccattccc cgggggnan aaaccgggac ngaagatttc
 W--> 367 420aanaccgcg ctntnattt taccnnggg nnngcgggtc gncccccncn nnacnngtga
 W--> 368 480naangggggg ctnttcaaann ttctnngtgc tnancacnac cctgggttt natantant
 W--> 369 540ncanaattnc gggnggaana ccaccgggc ttnannnctt nnaacnggnnc nnncnacccnn
 W--> 370 600ctttccnnnn ngggggggng ttccnnccnc cccccntttnn ntnntttnn aaanntttt
 E--> 371 660ggggaaaaaa aa 672

373 <210> SEQ ID NO: 15
 374 <211> LENGTH: 1676
 375 <212> TYPE: DNA
 376 <213> ORGANISM: Psuedomonas fluorescens
 378 <220> FEATURE:
 379 <221> NAME/KEY: variation
 380 <222> LOCATION: (1)...(1676)
 381 <223> OTHER INFORMATION: n is a, t, c, or g.
 383 <400> SEQUENCE: 15

E--> 384 tgcttgtgttaaagatcagg gccccgncc nccnnantta ngtctgggtc aacgacacnn
 W--> 385 60catnggtgcn gtgnanctc antttacnag gcncattaa ngtatnattt ttatnacgtn
 W--> 386 120ngncgaggtn gntcctcccn tancgaaagn natntgnna cttgaaanga tttnancntt

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W--> 387 180ttccantcgg tngntaccag nnngtgcantcn tcantttctg acaccnctg gtnncnnntcc
W--> 388 240tgttcaacncc tananngac cnctctcgn gntgngggcc tggngcntaa tatnntaccg
W--> 389 300gcttnnnt gctgtcaga tnanctcgn nacngnnaaa ntcnctcnc annccgtgt
W--> 390 360tntngtctcn cncttctcet ntcnctacac tcactnactn tntnctgnna atcnntctnn
W--> 391 420ctgtantatc acggncancn cgttctntgt ggggctcnct tganaggctc cccctnacact
W--> 392 480ctctannnac ngtgtcggtt atnnnctat aanagtcttg tgcatgtntc acagtnacat
W--> 393 540cgtcgccnnn cnccngtagc tctgcatcnt cgccctttt tttctnttct ctengcaan
W--> 394 600atcttnntnt ctctcnntcn atcattattc ncangcgnng gggctccnt ccccctcnnn
W--> 395 660ncntcngttc nanacangtc ntnttttagct atgtcttatg tncnctntc anttttntn
W--> 396 720cncttcnac ncttcagann ggctnngnct gacctctata gtcgntcnc tcctccctct
W--> 397 780nctnntctct cngcnataac gcncnncnc ttctggnc tcnnngctc tnntnntata
W--> 398 840tccnnccn nttctctcta tctctccgnt htgtgctcnt caattgtncn ctctctcgtn
W--> 399 900cnncgtcnn ntctancgtt ttcttgactt nannaatacn tacctctt ngcctctcn
W--> 400 960cntntnctct cnccgcacatc cttnngacgc tncctctgcn cngegcnac tcttcttnc
W--> 401 1020gttctccnnt tctcgcnct ctctnnngtac tngctttcc cnctacctnt ctcttgcctcc
W--> 402 1080ttcctcgcnt cntctncctc tctcttctct ntctangtcn ncncgnccat nggcttctc
W--> 403 1140tcgctcnntn tcnctcttct ntctntnccg tctcgctcng atcnntctct catcatnnc
W--> 404 1200tntntntca tcangcttn tgnactc tnatctgtt ctctnttta ntntnccntc
W--> 405 1260cttcctnntc tcttanctcn cgtnnatnnc ntctctgtat ntctcnagt atntctatgt
W--> 406 1320acgctnnnent tnatcgngnn cctntctcta tcancatcat ntagctnnnc ttccatngt
W--> 407 1380cctgctctca ctntttctgc cnanatatnn atcnctnctc tntatcttcn tanattnntn
W--> 408 1440cctntnaatg tttnanaatg ctctactcna nctctntn tcttnnnctc cagntcactc
W--> 409 1500tctananntg cctnnngtta tacgntcttn tncgctttan tgcgtntnct atcantnncg
W--> 410 1560ctctttntt ctctctcnc cngtntcttn ncacactnct ttcatcttct ctcnnatatn
E--> 411 1620natgtcnntc tatnnccnct tctatgctnt cnccntcna nccacantnt nntctc 1676

413 <210> SEQ ID NO: 16
414 <211> LENGTH: 721
415 <212> TYPE: DNA
416 <213> ORGANISM: Psuedomonas fluorescens
418 <220> FEATURE:
419 <221> NAME/KEY: variation
420 <222> LOCATION: (1)...(721)
421 <223> OTHER INFORMATION: n is a, t, c, or g.
423 <400> SEQUENCE: 16

E--> 424 tncttggtta taagatcagg cctatngccg nctgnggntt ntctgggtgc ncgacgcgcc
W--> 425 60attcgaaaaa ancagctccg nnaccngttc caantacacn nnngtgcnn nccgnagttc
W--> 426 120cagcttcngc ctcgcccnaacg tnnacaattc ctncnaaacc ctgggtgtgn tnttccnnna
W--> 427 180gctnatgtan ganngtgcna ngnctgnnn gnactgtcnt accnagnncn angtnggcac
W--> 428 240caaccngagc ntcattcncg cnnaacncga accccngng natcgcttct ntccnaacnc
W--> 429 300cnncnaatcc aacnccatng gttgtgtgn cnacgacnng ngcggaaaacn ncgcncacnn
W--> 430 360ngnccnagtc aagttcccgc ataccacag cnggtcnggg ggtntcnccc cctntctgt
W--> 431 420tccaaacatn nccatanaan nnngtntg ctgggggaat ccaanccntc nnctgngggtt
W--> 432 480cgatcnaaac aanaatanggg tcaanggnncn gccacttgcn tnatnaattt cnncagtgcc
W--> 433 540cnctnnctnc tgatnngcna agccnccnnn gggttggngg gggnnnttnc cnnnntatna
W--> 434 600antanaaaacg gcnngntcnn tnnccnccan gggtgnttg ngnttnnaa aacnncttt
E--> 435 660nnnnnaaan ccccccncct nttnccnng gannannatc cnnaaannnn gttccnnccc
E--> 436 721

720c

438 <210> SEQ ID NO: 17
439 <211> LENGTH: 452

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440 <212> TYPE: DNA
 441 <213> ORGANISM: Psuedomonas fluorescens
 443 <220> FEATURE:
 444 <221> NAME/KEY: variation
 445 <222> LOCATION: (1)...(452)
 446 <223> OTHER INFORMATION: n is a, t, c, or g.
 448 <400> SEQUENCE: 17
 E--> 449 atnnngnnnn tncttgta taagntcagg gcncncnctn tcnnaacttn gtctgggtcg
 W--> 450 60ngctacacnn cannggnac tggcagctcg gtnaccgcta cctnanaacg cttcantgtt
 W--> 451 120cctcagcngg tccacgtcca gccttgcgac acatgtnaaa annncngccna caanccnngg
 W--> 452 180ngtnaanntc cacgnnntgc ncgacgantg ccaatnnaan nttctcnacn gtttcacctg
 W--> 453 240gaangacctt gccganacccn anacnntcac caanggtgaa nncaactccc ggnagatncg
 W--> 454 300ctncacnccn gacccccaaacg aatcctncgc cgnnggttt nttagcanca tcgnncgncan
 W--> 455 360caaccangnc canttcnccc cgntntcatt ccnnccnanc gacggnnnnt ctgggcgtcn
 E--> 456 420cccccccgta actantctac ncntnncaaa aa 452
 458 <210> SEQ ID NO: 18
 459 <211> LENGTH: 442
 460 <212> TYPE: DNA
 461 <213> ORGANISM: Psuedomonas fluorescens
 463 <220> FEATURE:
 464 <221> NAME/KEY: variation
 465 <222> LOCATION: (1)...(422)
 466 <223> OTHER INFORMATION: n is a, t, c, or g.
 468 <400> SEQUENCE: 18
 E--> 469 tncttgta taagntcagg ntctnagatg agctcggtag ttcangagnt tttctgcgac
 W--> 470 60cgcggnncgg acgnctgnaa tcgntggcna ggttngccta nacannnnaa agtannnc
 W--> 471 120tcgaancngt cnntgaccc tcgtntccaaa tngtacngt cattggncga cgcnnncnca
 W--> 472 180cccnncactt cgctcgacnt cccaaannc gcctggccn ngcncgncng gattnngccc
 W--> 473 240gacatcnct nancaaantn ccccnccgcn tactngncca nccttgacca nntttgnc
 W--> 474 300tcctntcctt actgggtcng ctgcgtccc ggnttgcna ccannatggt ccnaancctg
 W--> 475 360ctgtccnca ctctcaaattn cggcccccggc caaccntgct gatcgncncc nncnccnag
 E--> 476 420tnctattcaa cccctgcccc aa 442
 478 <210> SEQ ID NO: 19
 479 <211> LENGTH: 538
 480 <212> TYPE: DNA
 481 <213> ORGANISM: Psuedomonas fluorescens
 483 <220> FEATURE:
 484 <221> NAME/KEY: variation
 485 <222> LOCATION: (1)...(538)
 486 <223> OTHER INFORMATION: n is a, t, c, or g.
 488 <400> SEQUENCE: 19
 E--> 489 ctttgttata taagnatcag acactagagc ttgccttc tncancnctt cnatggacag
 W--> 490 60cggtttcgg gcccgtcgagc aacgatctgt ccacagttna ncaccannag gcgntccacc
 W--> 491 120atcaanagaa aggannncng gtnctnacc acnnacacan gtcttgattnat cnaccacggc
 W--> 492 180agccaagcgn tggttcaaac gttctcagc ngttgcgtcc atggatctgg ttgggtcg
 W--> 493 240caanaacaag ataggcgtgt tnancnccnt ncnactngac acgtggaaat tntngctcta
 W--> 494 300accncccgac angttctgtc nncnctncc naatnnnaat tcataacctt ncngatgccn
 W--> 495 360cgccccaaat tcatnncncc cccgcanttc acggntggaa acacanttca actncnacgt
 W--> 496 420ttcnggcgccc naaaantttt gttgtcncncc aggnntnnm nancancnng atntttttgg

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E--> 497 480gggncccttnc cnaantttttt nnnccnctcc cntnannttg aanntngnng gatgttna

538

499 <210> SEQ ID NO: 20

500 <211> LENGTH: 218

501 <212> TYPE: DNA

502 <213> ORGANISM: Psuedomonas fluorescens

504 <220> FEATURE:

505 <221> NAME/KEY: variation

506 <222> LOCATION: (1)...(218)

507 <223> OTHER INFORMATION: n is a, t, c, or g.

509 <400> SEQUENCE: 20

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

E--> 510 tnatttgtataaggtcag gttgctngt gnacccatc ccggccaagg gttgccggcg

W--> 511 60tcacccacat ngtactagtc nnccgcgtggc cnaaacggtg angtctncta attgatgctt

W--> 512 120gccaacgntt naaaaaaaaaaaag tatngacagg gtnttaacca tcagnttnn ccnaaangta

E--> 513 180ctagtctacc cgtggccana naantnnann nntggnc

218

686 <210> SEQ ID NO: 34

687 <211> LENGTH: 595

688 <212> TYPE: PRT

689 <213> ORGANISM: Escherichia coli

691 <400> SEQUENCE: 34

692 Met Ala Gln Val Ile Asn Thr Asn Ser Leu Ile Thr Gln Asn 1

E--> 693 5 10 15 Asn Ile Asn Lys Asn Gln Ser Ala Sample
694 Leu Ser Ser Ser Ile Glu Arg Leu 20 25 provided at
E--> 695 30 Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Gly Gln
E--> 696 35 40 45 Ala Ile Ala Asn Arg Phe
697 Thr Ser Asn Ile Lys Gly Leu Thr Gln Ala 50 55
E--> 698 60 Ala Arg Asn Ala Asn Asp Gly Ile Ser Val Ala Gln Thr Thr Glu
E--> 699 Gly65 70 75 80 Ala Leu Ser
700 Glu Ile Asn Asn Leu Gln Arg Ile Arg Glu Leu Thr 85
E--> 701 90 95 Val Gln Ala Ser Thr Gly Thr Asn Ser Asp Ser Asp Leu
E--> 702 Asp Ser Ile 100 105 110 Gln
703 Asp Glu Ile Lys Ser Arg Leu Asp Glu Ile Asp Arg Val Ser Gly 115
E--> 704 120 125 Gln Thr Gln Phe Asn Gly Val Asn Val Leu Ala
705 Lys Asp Gly Ser Met 130 135 140
706 Lys Ile Gln Val Gly Ala Asn Asp Gly Gln Thr Ile Thr Ile Asp Leu 145
E--> 707 150 155 160 Lys Lys Ile Asp Ser Asp Thr Leu Gly
708 Leu Asn Gly Phe Asn Val Asn 165 170
E--> 709 175 Gly Ser Gly Thr Ile Ala Asn Lys Ala Ala Thr Ile Ser Asp Leu Thr
E--> 710 180 185 190 Ala Ala Lys Met Asp Ala Ala
711 Thr Asn Thr Ile Thr Thr Asn Asn 195 200
E--> 712 205 Ala Leu Thr Ala Ser Lys Ala Leu Asp Gln Leu Lys Asp Gly Asp Thr
E--> 713 210 215 220 Val Thr Ile Lys Ala
714 Asp Ala Ala Gln Thr Ala Thr Val Tyr Thr Tyr 225 230
E--> 715 235 240 Asn Ala Ser Ala Gly Asn Phe Ser Phe Ser Asn Val Ser Asn
E--> 716 Asn Thr 245 250 255 Ser Ala
717 Lys Ala Gly Asp Val Ala Ala Ser Leu Leu Pro Pro Ala Gly 260
E--> 718 265 270 Gln Thr Ala Ser Gly Val Tyr Lys Ala Ala Ser Gly
719 Glu Val Asn Phe 275 280 285
720 Asp Val Asp Ala Asn Gly Lys Ile Thr Ile Gly Gly Gln Glu Ala Tyr 290
E--> 721 295 300 Leu Thr Ser Asp Gly Asn Leu Thr Thr Asn

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722 Asp Ala Gly Gly Ala Thr	305	310	315
E--> 723 320Ala Ala Thr Leu Asp Gly Leu Phe Lys Lys Ala Gly Asp Gly Gln Ser			
E--> 724 325	330	335	Ile Gly Phe Asn Lys Thr Ala Ser
725 Val Thr Met Gly Gly Thr Thr Tyr		340	345
E--> 726 350	Asn Phe Lys Thr Gly Ala Asp Ala Gly Ala Ala Thr Ala Asn Ala Gly		
E--> 727 355	360	365	Val Ser Phe Thr Asp Thr
728 Ala Ser Lys Glu Thr Val Leu Asn Lys Val		370	375
E--> 729 380	Ala Thr Ala Lys Gln Gly Thr Ala Val Ala Ala Asn Gly Asp Thr		
E--> 730 Ser385	390	395	400Ala Thr Ile
731 Thr Tyr Lys Ser Gly Val Gln Thr Tyr Gln Ala Val Phe			405
E--> 732 410	415	Ala Ala Gly Asp Gly Thr Ala Ser Ala Lys Tyr Ala Asp	
E--> 733 Asn Thr Asp	420	425	430 Val
734 Ser Asn Ala Thr Ala Thr Tyr Thr Asp Ala Asp Gly Glu Met Thr			435
E--> 735 440	445	Thr Ile Gly Ser Tyr Thr Thr Lys Tyr Ser Ile	
736 Asp Ala Asn Asn Gly	450	455	460
737 Lys Val Thr Val Asp Ser Gly Thr Gly Ser Gly Lys Tyr Ala Pro Lys			465
E--> 738 470	475	480Val Gly Ala Glu Val Tyr Val Ser Ala	
739 Asn Gly Thr Leu Thr Thr Asp		485	490
E--> 740 495	Ala Thr Ser Glu Gly Thr Val Thr Lys Asp Pro Leu Lys Ala Leu Asp		
E--> 741 500	505	510	Glu Ala Ile Ser Ser Ile Asp
742 Lys Phe Arg Ser Ser Leu Gly Ala Ile		515	520
E--> 743 525	Gln Asn Arg Leu Asp Ser Ala Val Thr Asn Leu Asn Asn Thr Thr		
E--> 744 530	535	540	Asn Leu Ser Glu Ala
745 Gln Ser Arg Ile Gln Asp Ala Asp Tyr Ala Thr			545 550
E--> 746 555	560Glu Val Ser Asn Met Ser Lys Ala Gln Ile Ile Gln Gln Ala		
E--> 747 Gly Asn	565	570	575 Ser Val
748 Leu Ala Lys Ala Asn Gln Val Pro Gln Gln Val Leu Ser Leu			580
E--> 749 585	590	Leu Gln Gly	595
751 <210> SEQ ID NO: 35			
752 <211> LENGTH: 119			
753 <212> TYPE: PRT			
754 <213> ORGANISM: Escherichia coli			
756 <400> SEQUENCE: 35			
757 Met Gly Ile Met His Thr Ser Glu Leu Lys His Ile Tyr Asp Ile 1			
E--> 758 5	10	15	Asn Leu Ser Tyr Leu Leu Ala
759 Gln Arg Leu Ile Val Gln Asp Lys		20	25
E--> 760 30	Ala Ser Ala Met Phe Arg Leu Gly Ile Asn Glu Glu Met Ala Thr Thr		
E--> 761 35	40	45	Leu Ala Ala Leu Thr Leu
762 Pro Gln Met Val Lys Leu Ala Glu Thr Asn		50	55
E--> 763 60	Gln Leu Val Cys His Phe Arg Phe Asp Ser His Gln Thr Ile Thr		
E--> 764 Gln65	70	75	80 Leu Thr Gln
765 Asp Ser Arg Val Asp Asp Leu Gln Gln Ile His Thr Gly			85
E--> 766 90	95	Ile Met Leu Ser Thr Arg Leu Leu Asn Asp Val Asn Gln	
E--> 767 Pro Glu Glu	100	105	110 Ala
E--> 768 Leu Arg Lys Lys Arg Ala	115		
770 <210> SEQ ID NO: 36			
771 <211> LENGTH: 295			
772 <212> TYPE: PRT			
773 <213> ORGANISM: Escherichia coli			

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775 <400> SEQUENCE: 36
 776 Met Leu Ile Leu Leu Gly Tyr Leu Val Val Leu Gly Thr Val Phe Gly 1
 E--> 777 5 10 15 Gly Tyr Leu Met Thr Gly Gly Ser
 778 Leu Gly Ala Leu Tyr Gln Pro Ala 20 25
 E--> 779 30 Glu Leu Val Ile Ile Ala Gly Ala Gly Ile Gly Ser Phe Ile Val Gly
 E--> 780 35 40 45 Asn Asn Gly Lys Ala Ile
 781 Lys Gly Thr Leu Lys Ala Leu Pro Leu Leu 50 55
 E--> 782 60 Phe Arg Arg Ser Lys Tyr Thr Lys Ala Met Tyr Met Asp Leu Leu
 E--> 783 Ala65 70 75 80 Leu Leu Tyr
 784 Arg Leu Met Ala Lys Ser Arg Gln Met Gly Met Phe Ser 85
 E--> 785 90 95 Leu Glu Arg Asp Ile Glu Asn Pro Arg Glu Ser Glu Ile
 E--> 786 Phe Ala Ser 100 105 110 Tyr
 787 Pro Arg Ile Leu Ala Asp Ser Val Met Leu Asp Phe Ile Val Asp 115
 E--> 788 120 125 Tyr Leu Arg Leu Ile Ile Ser Gly His Met Asn
 789 Thr Phe Glu Ile Glu 130 135 140
 790 Ala Leu Met Asp Glu Glu Ile Glu Thr His Glu Ser Glu Ala Glu Val 145
 E--> 791 150 155 160 Pro Ala Asn Ser Leu Ala Leu Val Gly
 792 Asp Ser Leu Pro Ala Phe Gly 165 170
 E--> 793 175 Ile Val Ala Ala Val Met Gly Val Val His Ala Leu Gly Ser Ala Asp
 E--> 794 180 185 190 Arg Pro Ala Ala Glu Leu Gly
 795 Ala Leu Ile Ala His Ala Met Val Gly 195 200
 E--> 796 205 Thr Phe Leu Gly Ile Leu Leu Ala Tyr Gly Phe Ile Ser Pro Leu Ala
 E--> 797 210 215 220 Thr Val Leu Arg Gln
 798 Lys Ser Ala Glu Thr Ser Lys Met Met Gln Cys 225 230
 E--> 799 235 240 Val Lys Val Thr Leu Leu Ser Asn Leu Asn Gly Tyr Ala Pro
 E--> 800 Pro Ile 245 250 255 Ala Val
 801 Glu Phe Gly Arg Lys Thr Leu Tyr Ser Ser Glu Arg Pro Ser 260
 E--> 802 265 270 Phe Ile Glu Leu Glu His Val Arg Ala Val Lys
 803 Asn Pro Gln Gln 275 280 285
 E--> 804 Gln Thr Thr Glu Ala 290 295
 806 <210> SEQ ID NO: 37
 807 <211> LENGTH: 308
 808 <212> TYPE: PRT
 809 <213> ORGANISM: Escherichia coli
 811 <400> SEQUENCE: 37
 812 Met Lys Asn Gln Ala His Pro Ile Ile Val Val Lys Arg Arg Lys Ala 1
 E--> 813 5 10 15 Lys Ser His Gly Ala Ala His Gly
 814 Ser Trp Lys Ile Ala Tyr Ala Asp 20 25
 E--> 815 30 Phe Met Thr Ala Met Met Ala Phe Phe Leu Val Met Trp Leu Ile Ser
 E--> 816 35 40 45 Ile Ser Ser Pro Lys Glu
 817 Leu Ile Gln Ile Ala Glu Tyr Phe Arg Thr 50 55
 E--> 818 60 Pro Leu Ala Thr Ala Val Thr Gly Gly Asp Arg Ile Ser Asn Ser
 E--> 819 Glu65 70 75 80 Ser Pro Ile
 820 Pro Gly Gly Gly Asp Asp Tyr Thr Gln Ser Gln Gly Glu 85
 E--> 821 90 95 Val Asn Lys Gln Pro Asn Ile Glu Glu Leu Lys Lys Arg
 E--> 822 Met Glu Gln 100 105 110 Ser
 823 Arg Leu Arg Lys Leu Arg Gly Asp Leu Asp Gln Leu Ile Glu Ser 115
 E--> 824 120 125 Asp Pro Lys Leu Arg Ala Leu Arg Pro His Leu
 825 Lys Ile Asp Leu Val 130 135 140

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Input Set : A:\Ep.txt
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826 Gln Glu Gly Leu Arg Ile Gln Ile Ile Asp Ser Gln Asn Arg Pro Met145
E--> 827 150 155 160Phe Arg Thr Gly Ser Ala Asp Val Glu
828 Pro Tyr Met Arg Asp Ile Leu 165 170
E--> 829 175 Arg Ala Ile Ala Pro Val Leu Asn Gly Ile Pro Asn Arg Ile Ser Leu
E--> 830 180 185 190 Ser Gly His Thr Asp Asp Phe
831 Pro Tyr Ala Ser Gly Glu Lys Gly Tyr 195 200
E--> 832 205 Ser Asn Trp Glu Leu Ser Ala Asp Arg Ala Asn Ala Ser Arg Arg Glu
E--> 833 210 215 220 Leu Met Val Gly Gly
834 Leu Asp Ser Gly Lys Val Leu Arg Val Val Gly225 230
E--> 835 235 240Met Ala Ala Thr Met Arg Leu Ser Asp Arg Gly Pro Asp Asp
E--> 836 Ala Val 245 250 255 Asn Arg
837 Arg Ile Ser Leu Leu Val Leu Asn Lys Gln Ala Glu Gln Ala 260
E--> 838 265 270 Ile Leu His Glu Asn Ala Glu Ser Gln Asn Glu Pro
839 Val Ser Ala Leu 275 280 285
840 Glu Lys Pro Glu Val Ala Pro Gln Val Ser Val Pro Thr Met Pro Ser 290
E--> 841 295 300 Ala Glu Pro Arg305
843 <210> SEQ ID NO: 38
844 <211> LENGTH: 245
845 <212> TYPE: PRT
846 <213> ORGANISM: Escherichia coli
848 <400> SEQUENCE: 38
849 Met Arg Arg Leu Leu Ser Val Ala Pro Val Leu Leu Trp Leu Ile Thr 1
E--> 850 5 10 15 Pro Leu Ala Phe Ala Gln Leu Pro
851 Gly Ile Thr Ser Gln Pro Leu Pro 20 25
E--> 852 30 Gly Gly Gly Gln Ser Trp Ser Leu Pro Val Gln Thr Leu Val Phe Ile
E--> 853 35 40 45 Thr Ser Leu Thr Phe Ile
854 Pro Ala Ile Leu Leu Met Met Thr Ser Phe 50 55
E--> 855 60 Thr Arg Ile Ile Ile Val Phe Gly Leu Leu Arg Asn Ala Leu Gly
E--> 856 Thr65 70 75 80 Pro Ser Ala
857 Pro Pro Asn Gln Val Leu Leu Gly Leu Ala Leu Phe Leu 85
E--> 858 90 95 Thr Phe Phe Ile Met Ser Pro Val Ile Asp Lys Ile Tyr
E--> 859 Val Asp Ala 100 105 110 Tyr
860 Gln Pro Phe Ser Glu Glu Lys Ile Ser Met Gln Glu Ala Leu Glu 115
E--> 861 120 125 Lys Gly Ala Gln Pro Leu Arg Glu Phe Met Leu
862 Arg Gln Thr Arg Glu 130 135 140
863 Ala Asp Leu Gly Leu Phe Ala Arg Leu Ala Asn Thr Gly Pro Leu Gln145
E--> 864 150 155 160Gly Pro Glu Ala Val Pro Met Arg Ile
865 Leu Leu Pro Ala Tyr Val Thr 165 170
E--> 866 175 Ser Glu Leu Lys Thr Ala Phe Gln Ile Gly Phe Thr Ile Phe Ile Pro
E--> 867 180 185 190 Phe Leu Ile Ile Asp Leu Val
868 Ile Ala Ser Val Leu Met Ala Leu Gly 195 200
E--> 869 205 Met Met Met Val Pro Pro Ala Thr Ile Ala Leu Pro Phe Lys Leu Met
E--> 870 210 215 220 Leu Phe Val Leu Val
871 Asp Gly Trp Gln Leu Leu Val Gly Ser Leu Ala225 230
E--> 872 235 240Gln Ser Phe Tyr Ser 245
874 <210> SEQ ID NO: 39
875 <211> LENGTH: 375
876 <212> TYPE: PRT
877 <213> ORGANISM: Escherichia coli

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879 <400> SEQUENCE: 39
 880 Met Ile Arg Leu Ala Pro Leu Ile Thr Ala Asp Val Asp Thr Thr Thr 1
 E--> 881 5 10 15 Leu Pro Gly Gly Lys Ala Ser Asp
 882 Ala Ala Gln Asp Phe Leu Ala Leu 20 25
 E--> 883 30 Leu Ser Glu Ala Leu Ala Gly Glu Thr Thr Thr Asp Lys Ala Ala Pro
 E--> 884 35 40 45 Gln Leu Leu Val Ala Thr
 885 Asp Lys Pro Thr Thr Lys Gly Glu Pro Leu 50 55
 E--> 886 60 Ile Ser Asp Ile Val Ser Asp Ala Gln Gln Ala Asn Leu Leu Ile
 E--> 887 Pro65 70 75 80 Val Asp Glu
 888 Thr Pro Pro Val Ile Asn Asp Glu Gln Ser Thr Ser Thr 85
 E--> 889 90 95 Pro Leu Thr Thr Ala Gln Thr Met Ala Leu Ala Ala Val
 E--> 890 Ala Asp Lys 100 105 110 Asn
 891 Thr Thr Lys Asp Glu Lys Ala Asp Asp Leu Asn Glu Asp Val Thr 115
 E--> 892 120 125 Ala Ser Leu Ser Ala Leu Phe Ala Met Leu Pro
 893 Gly Phe Asp Asn Thr 130 135 140
 894 Pro Lys Val Thr Asp Ala Pro Ser Thr Val Leu Pro Thr Glu Lys Pro 145
 E--> 895 150 155 160 Thr Leu Phe Thr Lys Leu Thr Ser Glu
 896 Gln Leu Thr Thr Ala Gln Pro 165 170
 E--> 897 175 Asp Asp Ala Pro Gly Thr Pro Ala Gln Pro Leu Thr Pro Leu Val Ala
 E--> 898 180 185 190 Glu Ala Gln Ser Lys Ala Glu
 899 Val Ile Ser Thr Pro Ser Pro Val Thr 195 200
 E--> 900 205 Ala Ala Ala Ser Pro Leu Ile Thr Pro His Gln Thr Gln Pro Leu Pro
 E--> 901 210 215 220 Thr Val Ala Ala Pro
 902 Val Leu Ser Ala Pro Leu Gly Ser His Glu Trp 225 230
 E--> 903 235 240 Gln Gln Ser Leu Ser Gln His Ile Ser Leu Phe Thr Arg Gln
 E--> 904 Gly Gln 245 250 255 Gln Ser
 905 Ala Glu Leu Arg Leu His Pro Gln Asp Leu Gly Glu Val Gln 260
 E--> 906 265 270 Ile Ser Leu Lys Val Asp Asp Asn Gln Ala Gln Ile
 907 Gln Met Val Ser 275 280 285
 908 Pro His Gln His Val Arg Ala Ala Leu Glu Ala Ala Leu Pro Val Leu 290
 E--> 909 295 300 Arg Thr Gln Leu Ala Glu Ser Gly Ile Gln
 910 Leu Gly Gln Ser Asn Ile 305 310 315
 E--> 911 320 Ser Gly Glu Ser Phe Ser Gly Gln Gln Ala Ala Ser Gln Gln Gln
 E--> 912 325 330 335 Gln Ser Gln Arg Thr Ala Asn His
 913 Glu Pro Leu Ala Gly Glu Asp Asp 340 345
 E--> 914 350 Asp Thr Leu Pro Val Pro Val Ser Leu Gln Gly Arg Val Thr Gly Asn
 E--> 915 355 360 365 Ser Gly Val Asp Ile Phe
 E--> 916 Ala 370 375
 918 <210> SEQ ID NO: 40
 919 <211> LENGTH: 547
 920 <212> TYPE: PRT
 921 <213> ORGANISM: Escherichia coli
 923 <400> SEQUENCE: 40
 924 Met Ser Ser Leu Ile Asn Asn Ala Met Ser Gly Leu Asn Ala Ala Gln 1
 E--> 925 5 10 15 Ala Ala Leu Asn Thr Ala Ser Asn
 926 Asn Ile Ser Ser Tyr Asn Val Ala 20 25
 E--> 927 30 Gly Tyr Thr Arg Gln Thr Thr Ile Met Ala Gln Ala Asn Ser Thr Leu
 E--> 928 35 40 45 Gly Ala Gly Gly Trp Val
 929 Gly Asn Gly Val Tyr Val Ser Gly Val Gln 50 55

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```

E--> 930 60          Arg Glu Tyr Asp Ala Phe Ile Thr Asn Gln Leu Arg Ala Ala Gln
E--> 931 Thr65        70          75          80 Gln Ser Ser
932 Gly Leu Thr Ala Arg Tyr Glu Gln Met Ser Lys Ile Asp          85
E--> 933 90          95          Asn Met Leu Ser Thr Ser Thr Ser Ser Leu Ala Thr Gln
E--> 934 Met Gln Asp 100          105          110 Phe
935 Phe Thr Ser Leu Gln Thr Leu Val Ser Asn Ala Glu Asp Pro Ala          115
E--> 936 120          125          Ala Arg Gln Ala Leu Ile Gly Lys Ser Glu Gly
937 Leu Val Asn Gln Phe 130          135          140
938 Lys Thr Thr Asp Gln Tyr Leu Arg Asp Gln Asp Lys Gln Val Asn Ile145
E--> 939 150          155          160 Ala Ile Gly Ala Ser Val Asp Gln Ile
940 Asn Asn Tyr Ala Lys Gln Ile          165          170
E--> 941 175          Ala Ser Leu Asn Asp Gln Ile Ser Arg Leu Thr Gly Val Gly Ala Gly
E--> 942 180          185          190          Ala Ser Pro Asn Asn Leu Leu
943 Asp Gln Arg Asp Gln Leu Val Ser Glu          195          200
E--> 944 205          Leu Asn Gln Ile Val Gly Val Glu Val Ser Val Gln Asp Gly Gly Thr
E--> 945 210          215          220          Tyr Asn Ile Thr Met
946 Ala Asn Gly Tyr Ser Leu Val Gln Gly Ser Thr225          230
E--> 947 235          240 Ala Arg Gln Leu Ala Ala Val Pro Ser Ser Ala Asp Pro Ser
E--> 948 Arg Thr      245          250          255 Thr Val
949 Ala Tyr Val Asp Gly Thr Ala Gly Asn Ile Glu Ile Pro Glu          260
E--> 950 265          270          Lys Leu Leu Asn Thr Gly Ser Leu Gly Gly Ile Leu
951 Thr Phe Arg Ser 275          280          285
952 Gln Asp Leu Asp Gln Thr Arg Asn Thr Leu Gly Gln Leu Ala Leu Ala          290
E--> 953 295          300          Phe Ala Glu Ala Phe Asn Thr Gln His Lys
954 Ala Gly Phe Asp Ala Asn305          310          315
E--> 955 320 Gly Asp Ala Gly Glu Asp Phe Phe Ala Ile Gly Lys Pro Ala Val Leu
E--> 956 325          330          335          Gln Asn Thr Lys Asn Lys Gly Asp
957 Val Ala Ile Gly Ala Thr Val Thr          340          345
E--> 958 350          Asp Ala Ser Ala Val Leu Ala Thr Asp Tyr Lys Ile Ser Phe Asp Asn
E--> 959 355          360          365          Asn Gln Trp Gln Val Thr
960 Arg Leu Ala Ser Asn Thr Thr Phe Thr Val          370          375
E--> 961 380          Thr Pro Asp Ala Asn Gly Lys Val Ala Phe Asp Gly Leu Glu Leu
E--> 962 Thr385        390          395          400 Phe Thr Gly
963 Thr Pro Ala Val Asn Asp Ser Phe Thr Leu Lys Pro Val          405
E--> 964 410          415          Ser Asp Ala Ile Val Asn Met Asp Val Leu Ile Thr Asp
E--> 965 Glu Ala Lys 420          425          430          Ile
966 Ala Met Ala Ser Glu Glu Asp Ala Gly Asp Ser Asp Asn Arg Asn          435
E--> 967 440          445          Gly Gln Ala Leu Leu Asp Leu Gln Ser Asn Ser
968 Lys Thr Val Gly Gly 450          455          460
969 Ala Lys Ser Phe Asn Asp Ala Tyr Ala Ser Leu Val Ser Asp Ile Gly465
E--> 970 470          475          480 Asn Lys Thr Ala Thr Leu Lys Thr Ser
971 Ser Ala Thr Gln Gly Asn Val          485          490
E--> 972 495          Val Thr Gln Leu Ser Asn Gln Gln Ser Ile Ser Gly Val Asn Leu
E--> 973 500          505          510          Asp Glu Glu Tyr Gly Asn Leu
974 Gln Arg Phe Gln Gln Tyr Tyr Leu Ala          515          520
E--> 975 525          Asn Ala Gln Val Leu Gln Thr Ala Asn Ala Ile Phe Asp Ala Leu Ile
E--> 976 530          535          540          Asn Ile Arg545
978 <210> SEQ ID NO: 41
979 <211> LENGTH: 566

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980 <212> TYPE: PRT
 981 <213> ORGANISM: Psuedomonas aeruginosa
 983 <400> SEQUENCE: 41
 984 Met Asn Asp Ser Ile Gln Leu Ser Gly Leu Ser Arg Gln Leu Val Gln 1
 E--> 985 5 10 15 Ala Asn Leu Leu Asp Glu Lys Thr
 986 Ala Leu Gln Ala Gln Thr Gln Ala 20 25
 E--> 987 30 Gln Arg Asn Lys Leu Ser Leu Val Thr His Leu Val Gln Asn Lys Leu
 E--> 988 35 40 45 Val Ser Gly Leu Ala Leu
 989 Ala Glu Leu Ser Ala Glu Gln Phe Gly Ile 50 55
 E--> 990 60 Ala Tyr Cys Asp Leu Asn Ser Leu Asp Arg Glu Ser Phe Pro Arg
 E--> 991 Asp65 70 75 80 Ala Ile Ser
 992 Glu Lys Leu Val Arg Gln His Arg Val Ile Pro Leu Trp 85
 E--> 993 90 95 Arg Arg Gly Asn Lys Leu Phe Val Gly Ile Ser Asp Ala
 E--> 994 Ala Asn His 100 105 110 Gln
 995 Ala Ile Asn Asp Val Gln Phe Ser Thr Gly Leu Thr Glu Ala 115
 E--> 996 120 125 Ile Leu Val Glu Asp Asp Lys Leu Gly Leu Ala
 997 Ile Asp Lys Leu Phe 130 135 140
 998 Glu Asn Ala Thr Asp Gly Leu Ala Gly Leu Asp Asp Val Asp Leu Glu 145
 E--> 999 150 155 160Gly Leu Asp Val Gly Val Lys Glu Thr
 1000 Ser Gly Gln Glu Asp Thr Gly 165 170
 E--> 1001 175 Ala Glu Ala Asp Asp Ala Pro Val Val Arg Phe Val Asn Lys Met Leu
 E--> 1002 180 185 190 Leu Asp Ala Ile Lys Gly Gly
 1003 Ser Ser Asp Leu His Phe Glu Pro Tyr 195 200
 E--> 1004 205 Glu Lys Ile Tyr Arg Val Arg Phe Arg Thr Asp Gly Met Leu His Glu
 E--> 1005 210 215 220 Val Ala Lys Pro Pro
 1006 Ile Gln Leu Ala Ser Arg Ile Ser Ala Arg Leu 225 230
 E--> 1007 235 240Lys Val Met Ala Gly Leu Asp Ile Ser Glu Arg Arg Lys Pro
 E--> 1008 Gln Asp 245 250 255 Gly Arg
 1009 Ile Lys Met Arg Val Ser Lys Thr Lys Ser Ile Asp Phe Arg 260
 E--> 1010 265 270 Val Asn Thr Leu Pro Thr Leu Trp Gly Glu Lys Ile
 1011 Val Met Arg Ile 275 280 285
 1012 Leu Asp Ser Ser Ser Ala Gln Met Gly Ile Asp Ala Leu Gly Tyr Glu 290
 E--> 1013 295 300 Glu Asp Gln Lys Glu Leu Tyr Leu Ala Ala
 1014 Leu Lys Gln Pro Gln Gly 305 310 315
 E--> 1015 320Met Ile Leu Val Thr Gly Pro Thr Gly Ser Gly Lys Thr Val Ser Leu
 E--> 1016 325 330 335 Tyr Thr Gly Leu Asn Ile Leu Asn
 1017 Thr Thr Asp Ile Asn Ile Ser Thr 340 345
 E--> 1018 350 Ala Glu Asp Pro Val Glu Ile Asn Leu Glu Gly Ile Asn Gln Val Asn
 E--> 1019 355 360 365 Val Asn Pro Arg Gln Gly
 1020 Met Asp Phe Ser Gln Ala Leu Arg Ala Phe 370 375
 E--> 1021 380 Leu Arg Gln Asp Pro Asp Val Ile Met Val Gly Glu Ile Arg Asp
 E--> 1022 Leu 385 390 395 400Glu Thr Ala
 1023 Glu Ile Ala Ile Lys Ala Ala Gln Thr Gly His Met Val 405
 E--> 1024 410 415 Met Ser Thr Leu His Thr Asn Ser Ala Ala Glu Thr Leu
 E--> 1025 Thr Arg Leu 420 425 430 Leu
 1026 Asn Met Gly Val Pro Ala Phe Asn Leu Ala Thr Ser Val Asn Leu 435
 E--> 1027 440 445 Ile Ile Ala Gln Arg Leu Ala Arg Lys Leu Cys
 1028 Ser His Cys Lys Lys 450 455 460
 1029 Glu His Asp Val Pro Lys Glu Thr Leu Leu His Glu Gly Phe Pro Glu 465

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Input Set : A:\Ep.txt
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E--> 1030 470 475 480Glu Leu Ile Gly Thr Phe Lys Leu Tyr
1031 Ser Pro Val Gly Cys Asp His 485 490
E--> 1032 495 Cys Lys Asn Gly Tyr Lys Gly Arg Val Gly Ile Tyr Glu Val Val Lys
E--> 1033 500 505 510 Asn Thr Pro Ala Leu Gln Arg
1034 Ile Ile Met Glu Glu Gly Asn Ser Ile 515 520
E--> 1035 525 Glu Ile Ala Glu Gln Ala Arg Lys Glu Gly Phe Asn Asp Leu Arg Thr
E--> 1036 530 535 540 Ser Gly Leu Leu Lys
1037 Ala Met Gln Gly Ile Thr Ser Leu Glu Glu Val 545 550
E--> 1038 555 560Asn Arg Val Thr Lys Asp 565
1040 <210> SEQ ID NO: 42
1041 <211> LENGTH: 406
1042 <212> TYPE: PRT
1043 <213> ORGANISM: Psuedomonas aeruginosa
1045 <400> SEQUENCE: 42
1046 Met Ala Asp Lys Ala Leu Lys Thr Ser Val Phe Ile Trp Glu Gly Thr 1
E--> 1047 5 10 15 Asp Lys Lys Gly Ala Lys Val Lys
1048 Gly Glu Leu Thr Gly Gln Asn Pro 20 25
E--> 1049 30 Met Leu Val Lys Ala His Leu Arg Lys Gln Gly Ile Asn Pro Leu Lys
E--> 1050 35 40 45 Val Arg Lys Lys Gly Ile
1051 Ser Leu Leu Gly Ala Gly Lys Lys Val Lys 50 55
E--> 1052 60 Pro Met Asp Ile Ala Leu Phe Thr Arg Gln Met Ala Thr Met Met
E--> 1053 Gly 65 70 75 80 Ala Gly Val
1054 Pro Leu Leu Gln Ser Phe Asp Ile Ile Gly Glu Gly Phe 85
E--> 1055 90 95 Asp Asn Pro Asn Met Arg Lys Leu Val Asp Glu Ile Lys
E--> 1056 Gln Glu Val 100 105 110 Ser
1057 Ser Gly Asn Ser Leu Ala Asn Ser Leu Arg Lys Lys Pro Gln Tyr 115
E--> 1058 120 125 Phe Asp Glu Leu Tyr Cys Asn Leu Val Asp Ala
1059 Gly Glu Gln Ser Gly 130 135 140
1060 Ala Leu Glu Asn Leu Leu Asp Arg Val Ala Thr Tyr Lys Glu Lys Thr 145
E--> 1061 150 155 160Glu Ser Leu Lys Ala Lys Ile Lys Lys
1062 Ala Met Thr Tyr Pro Ile Ala 165 170
E--> 1063 175 Val Ile Ile Val Ala Leu Ile Val Ser Ala Ile Leu Ile Lys Val
E--> 1064 180 185 190 Val Pro Gln Phe Gln Ser Val
1065 Phe Glu Gly Phe Gly Ala Glu Leu Pro 195 200
E--> 1066 205 Ala Phe Thr Gln Met Ile Val Asn Leu Ser Glu Phe Met Gln Glu Trp
E--> 1067 210 215 220 Trp Phe Phe Ile Ile
1068 Leu Ala Ile Ala Ile Phe Gly Phe Ala Phe Lys 225 230
E--> 1069 235 240Glu Leu His Lys Arg Ser Gln Lys Phe Arg Asp Thr Leu Asp
E--> 1070 Arg Thr 245 250 255 Ile Leu
1071 Lys Leu Pro Ile Phe Gly Ile Val Tyr Lys Ser Ala Val 260
E--> 1072 265 270 Ala Arg Tyr Ala Arg Thr Leu Ser Thr Thr Phe Ala
1073 Ala Gly Val Pro 275 280 285
1074 Leu Val Asp Ala Leu Asp Ser Val Ser Gly Ala Thr Gly Asn Ile Val 290
E--> 1075 295 300 Phe Lys Asn Ala Val Ser Lys Ile Lys Gln
1076 Asp Val Ser Thr Gly Met 305 310 315
E--> 1077 320Gln Leu Asn Phe Ser Met Arg Thr Thr Ser Val Phe Pro Asn Met Ala
E--> 1078 325 330 335 Ile Gln Met Thr Ala Ile Gly Glu
1079 Glu Ser Gly Ser Leu Asp Glu Met 340 345
E--> 1080 350 Leu Ser Lys Val Ala Ser Tyr Tyr Glu Glu Val Asp Asn Ala Val

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E--> 1081 355 360 365 Asp Asn Leu Thr Thr Leu
 1082 Met Glu Pro Met Ile Met Ala Val Leu Gly 370 375
 E--> 1083 380 Val Leu Val Gly Gly Leu Ile Val Ala Met Tyr Leu Pro Ile Phe
 E--> 1084 Gln385 390 395 400Leu Gly Asn
 E--> 1085 Val Val Gly 405
 1087 <210> SEQ ID NO: 43
 1088 <211> LENGTH: 290
 1089 <212> TYPE: PRT
 1090 <213> ORGANISM: Psuedomonas aeruginosa
 1092 <400> SEQUENCE: 43
 1093 Met Pro Leu Leu Asp Tyr Leu Ala Ser His Pro Leu Ala Phe Val Leu 1
 E--> 1094 5 10 15 Cys Ala Ile Leu Leu Gly Leu Leu
 1095 Val Gly Ser Phe Leu Asn Val Val 20 25
 E--> 1096 30 Val His Arg Leu Pro Lys Met Met Glu Arg Asn Trp Lys Ala Glu Ala
 E--> 1097 35 40 45 Arg Glu Ala Leu Gly Leu
 1098 Glu Pro Glu Pro Lys Gln Ala Thr Tyr Asn 50 55
 E--> 1099 60 Leu Val Leu Pro Asn Ser Ala Cys Pro Arg Cys Gly His Glu Ile
 E--> 1100 Arg65 70 75 80 Pro Trp Glu
 1101 Asn Ile Pro Leu Val Ser Tyr Leu Ala Leu Gly Gly Lys 85
 E--> 1102 90 95 Cys Ser Ser Cys Lys Ala Ala Ile Gly Lys Arg Tyr Pro
 E--> 1103 Leu Val Glu 100 105 110 Leu
 1104 Ala Thr Ala Leu Leu Ser Gly Tyr Val Ala Trp His Phe Gly Phe 115
 E--> 1105 120 125 Thr Trp Gln Ala Gly Ala Met Leu Leu Thr
 1106 Trp Gly Leu Leu Ala 130 135 140
 1107 Met Ser Leu Ile Asp Ala Asp His Gln Leu Leu Pro Asp Val Leu Val 145
 E--> 1108 150 155 160Leu Pro Leu Leu Trp Leu Gly Leu Ile
 1109 Ala Asn His Phe Gly Leu Phe 165 170
 E--> 1110 175 Ala Ser Leu Asp Asp Ala Leu Phe Gly Ala Val Phe Gly Tyr Leu Ser
 E--> 1111 180 185 190 Leu Trp Ser Val Phe Trp Leu
 1112 Phe Lys Leu Val Thr Gly Lys Glu Gly 195 200
 E--> 1113 205 Met Gly Tyr Gly Asp Phe Lys Leu Leu Ala Met Leu Gly Ala Trp Gly
 E--> 1114 210 215 220 Gly Trp Gln Ile Leu
 1115 Pro Leu Thr Ile Leu Leu Ser Ser Leu Val Gly 225 230
 E--> 1116 235 240Ala Ile Leu Gly Val Ile Met Leu Arg Leu Arg Asn Ala Glu
 E--> 1117 Ser Gly 245 250 255 Thr Pro
 1118 Ile Pro Phe Gly Pro Tyr Leu Ala Ile Ala Gly Trp Ile Ala 260
 E--> 1119 265 270 Leu Leu Trp Gly Asp Gln Ile Thr Arg Thr Tyr Leu
 1120 Gln Phe Ala Gly 275 280 285
 E--> 1121 Phe Lys 290
 1123 <210> SEQ ID NO: 44
 1124 <211> LENGTH: 185
 1125 <212> TYPE: PRT
 1126 <213> ORGANISM: Psuedomonas aeruginosa
 1128 <400> SEQUENCE: 44
 1129 Met Leu Leu Lys Ser Arg His Arg Ser Leu His Gln Ser Gly Phe Ser 1
 E--> 1130 5 10 15 Met Ile Glu Val Leu Val Ala Leu
 1131 Leu Leu Ile Ser Ile Gly Val Leu 20 25
 E--> 1132 30 Gly Met Ile Ala Met Gln Gly Lys Thr Ile Gln Tyr Thr Ala Asp Ser
 E--> 1133 35 40 45 Val Glu Arg Asn Lys Ala

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1134 Ala Met Leu Gly Ser Asn Leu Leu Glu Ser 50 55
E--> 1135 60 Met Arg Ala Ser Pro Lys Ala Leu Tyr Asp Val Lys Asp Gln Met
E--> 1136 Ala65 70 75 80 Thr Gln Ser
1137 Asp Phe Phe Lys Ala Lys Gly Ser Ala Phe Pro Thr Ala 85
E--> 1138 90 95 Pro Ser Ser Cys Thr Pro Leu Pro Asp Ala Ile Lys Asp
E--> 1139 Arg Leu Gly 100 105 110 Cys
1140 Trp Ala Glu Gln Val Lys Asn Glu Leu Pro Gly Ala Gly Asp Leu 115
E--> 1141 120 125 Leu Lys Ser Asp Tyr Tyr Ile Cys Arg Ser Ser
1142 Lys Pro Gly Asp Cys 130 135 140
1143 Asp Gly Lys Gly Ser Met Leu Glu Ile Arg Leu Ala Trp Arg Gly Lys 145
E--> 1144 150 155 160Gln Gly Ala Cys Val Asn Ala Ala Asp
1145 Ser Ser Ala Asp Thr Ser Leu 165 170
E--> 1146 175 Cys Tyr Tyr Thr Leu Arg Val Glu Pro 180 185
1148 <210> SEQ ID NO: 45
1149 <211> LENGTH: 274
1150 <212> TYPE: PRT
1151 <213> ORGANISM: Psuedomonas aeruginosa
1153 <400> SEQUENCE: 45
1154 Met Ser Met Asn Asn Arg Ser Arg Arg Gln Ser Gly Leu Ser Met Ile 1
E--> 1155 5 10 15 Glu Leu Leu Val Ala Leu Ala Ile
1156 Ser Ser Phe Leu Ile Leu Gly Ile 20 25
E--> 1157 30 Thr Gln Ile Tyr Leu Asp Asn Lys Arg Asn Tyr Leu Phe Gln Gln Gly
E--> 1158 35 40 45 Gln Ala Gly Asn Gln Glu
1159 Asn Gly Arg Phe Ala Met Met Phe Leu Asp 50 55
E--> 1160 60 Gln Gln Leu Ala Lys Val Gly Phe Arg Arg Arg Ala Asp Asp Pro
E--> 1161 Asn65 70 75 80 Glu Phe Ala
1162 Phe Pro Ala Gln Gln Lys Thr Ala Tyr Cys Glu Ala Phe 85
E--> 1163 90 95 Lys Ala Gly Ser Thr Leu Val Pro Ala Val Val Lys Ala
E--> 1164 Gly Gln Ser 100 105 110 Gly
1165 Phe Cys Tyr Arg Tyr Gln Pro Ala Pro Gly Glu Ala Tyr Asp Cys 115
E--> 1166 120 125 Glu Gly Asn Ser Ile Thr Thr Pro Ser Asp Pro
1167 Phe Ala Thr Ala Gln 130 135 140
1168 Ala Ile Thr Ala Arg Val Leu Phe Val Pro Ala Thr Ala Asp Val Pro 145
E--> 1169 150 155 160Gly Ser Leu Ala Cys Ser Ala Gln Thr
1170 Ile Lys Glu Lys Gly Gln Glu 165 170
E--> 1171 175 Ile Val Ser Gly Leu Val Asp Phe Lys Leu Glu Tyr Gly Val Gly Pro
E--> 1172 180 185 190 Thr Met Ala Gly Lys Arg Glu
1173 Val Glu Ser Phe Val Glu Gln Ala Asn 195 200
E--> 1174 205 Ile Ala Asp Arg Pro Val Arg Ala Leu Arg Tyr Ser Ala Leu Met Ala
E--> 1175 210 215 220 Ser Asp Lys Asn Leu
1176 Arg Gln Gly Asp Ser Lys Thr Leu Asp Asp Trp 225 230
E--> 1177 235 240Ile Thr Leu Tyr Pro Ser Ser Lys Thr Ser Leu Gln Gly Asn
E--> 1178 Asp Lys 245 250 255 Asp Arg
1179 Leu Tyr Gln Ile Ala Lys Gly Ser Gln Thr Leu Arg Asn Leu 260
E--> 1180 265 270 Val Pro
1182 <210> SEQ ID NO: 46
1183 <211> LENGTH: 172
1184 <212> TYPE: PRT
1185 <213> ORGANISM: Psuedomonas aeruginosa

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1187 <400> SEQUENCE: 46
 1188 Met Asn Asn Phe Pro Ala Gln Gln Arg Gly Ala Thr Leu Val Ile Ala 1
 E--> 1189 5 10 15 15 Leu Ala Ile Leu Val Ile Val Thr
 1190 Leu Leu Ala Val Ser Ser Met Arg 20 20 25
 E--> 1191 30 30 30 30 Glu Val Val Leu Glu Ser Arg Ile Thr Gly Asn Val Ile Glu Gln Thr
 E--> 1192 35 40 45 45 Arg Leu Gln Asn Ala Ala
 1193 Glu Ser Gly Leu Arg Glu Gly Glu Arg Arg 50 50 55
 E--> 1194 60 60 60 60 Phe Val Asn Thr Leu Arg Pro Pro Glu Pro Gly Thr Gly Cys Thr
 E--> 1195 Ala65 70 75 75 80 Asp Asn Val
 1196 Ala Arg Pro Cys Leu Leu Asp Leu Ala Ala Leu Asn Leu 85
 E--> 1197 90 90 95 95 Lys Leu Ala Asp Thr His Gln Asn Pro Val Gly Val Leu
 E--> 1198 Lys Gly Ile 100 100 105 110 Ala
 1199 Asn Thr Trp Met Ser Tyr Arg Gly Ser Asp Ile Ser Ser Ala Thr 115
 E--> 1200 120 120 125 125 Thr Ala Gly Asn Ala Leu Gln Arg Ala Val Glu
 1201 Gln Pro Ala His Ser 130 130 135 140
 1202 Leu Gly Arg Pro Gly Gln Arg Ser Gly Lys Pro Arg Ile Arg Gln Pro 145
 E--> 1203 150 150 155 155 160Asp Ala Arg His Arg His Leu Leu Leu
 E--> 1204 Arg Asp Gln 165 165 170
 1206 <210> SEQ ID NO: 47
 1207 <211> LENGTH: 1161
 1208 <212> TYPE: PRT
 1209 <213> ORGANISM: Psuedomonas aeruginosa
 1211 <400> SEQUENCE: 47
 1212 Met Arg Gly Ile Gly Thr Phe Tyr Tyr Glu Thr Asn Ser Val Ala Arg 1
 E--> 1213 5 10 10 15 Asn Gln Thr Asn Ser Glu Thr Val
 1214 Leu Gln Thr Val Ala Arg Pro Ser 20 20 25
 E--> 1215 30 30 30 30 Leu Tyr Gln Leu Ile Glu Pro Arg Met Lys Ser Val Leu His Gln Ile
 E--> 1216 35 40 40 45 Gly Lys Thr Ser Leu Ala
 1217 Ala Ala Leu Ser Gly Ala Val Leu Leu Ser 50 50 55
 E--> 1218 60 60 60 60 Ala Gln Thr Thr His Ala Ala Ala Leu Ser Val Ser Gln Gln Pro
 E--> 1219 Leu65 70 70 75 80 Met Leu Ile
 1220 Gln Gly Val Ala Pro Asn Met Leu Val Thr Leu Asp Asp 85
 E--> 1221 90 90 95 95 Ser Gly Ser Met Ala Phe Ala Tyr Ala Pro Asp Ser Ile
 E--> 1222 Ser Gly Tyr 100 100 105 110 Gly
 1223 Asn Tyr Thr Phe Phe Ala Ser Asn Ser Phe Asn Pro Met Tyr Phe 115
 E--> 1224 120 120 125 125 Asp Pro Asn Thr Gln Tyr Lys Leu Pro Lys Lys
 1225 Leu Thr Leu Val Asn 130 130 135 140
 1226 Gly Gln Val Gln Ile Gln Asp Tyr Pro Ala Pro Asn Phe Ser Ser Ala 145
 E--> 1227 150 150 155 155 160Trp Arg Asn Gly Phe Thr Arg Arg Gly
 1228 Ser Ile Asn Leu Ser Asn Ser 165 165 170
 E--> 1229 175 175 175 175 Tyr Lys Val Thr Ile Glu Tyr Gly Arg Gly Tyr Asp Lys Glu Ser Thr
 E--> 1230 180 180 185 185 Ile Lys Ala Asp Ala Ala Tyr
 1231 Tyr Tyr Asp Phe Thr Gly Ser Ser Ser 195 195 200
 E--> 1232 205 205 205 205 Trp Asn Arg Thr Asn Gln Ala Cys Tyr Thr Arg Arg Tyr Val Ser Thr
 E--> 1233 210 210 215 215 Glu Gln Arg Gln Asn
 1234 Phe Ala Asn Trp Tyr Ser Phe Tyr Arg Thr Arg 225 230
 E--> 1235 235 235 240Ala Leu Arg Thr Gln Thr Ala Ala Asn Leu Ala Phe Phe Arg
 E--> 1236 Leu Pro 245 245 250 255 Glu Asn
 1237 Ala Arg Val Ser Trp Gln Leu Leu Asn Asp Ser Asn Cys Asn 260

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E--> 1238 265	270	Gln Met Gly Ser Gly Ser Arg Leu Arg Gln Leu Phe
1239 Gln Gln Leu Ser	275	280 285
1240 Thr Gly Leu His Arg Ser Thr Ala Gly Glu Leu Leu Gln Leu Ala Gly		290
E--> 1241 295	300	Lys Thr Phe Gly Gln Trp Trp Tyr Ala Leu
1242 Arg Gln Ala Met Thr Arg	305	310 315
E--> 1243 320Glu Ala Ser Phe Ser Arg Arg Pro Ala Ser Asn Gly Pro Tyr Ala Tyr		
E--> 1244 325	330	335 Arg Pro Gly Thr Gln Thr Ala Pro
1245 Glu Tyr Ser Cys Arg Gly Ser Tyr		340 345
E--> 1246 350	His Ile Leu Met Thr Asp Gly Leu Trp Asn Asn Asp Ser Ala Asn Val	
E--> 1247 355	360	365 Gly Asn Ala Asp Ser Thr
1248 Ala Arg Asn Leu Pro Asp Gly Lys Ser Tyr		370 375
E--> 1249 380	Ser Ser Gln Thr Pro Tyr Arg Asp Gly Thr Phe Asp Thr Leu Ala	
E--> 1250 Asp385	390	395 400Gln Ala Phe
1251 His Tyr Trp Ala Thr Asp Ala Arg Pro Asp Ile Asp Asp		405
E--> 1252 410	415	Asn Ile Lys Pro Tyr Ile Pro Tyr Pro Asp Gln Asp Asn
E--> 1253 Pro Ser Gly	420	425 430 Glu
1254 Tyr Trp Asn Pro Arg Asn Asp Pro Ala Ile Trp Gln His Met Val		435
E--> 1255 440	445	Thr Tyr Thr Leu Gly Leu Gly Leu Asn Thr Ser
1256 Leu Thr Ser Pro Arg	450	455 460
1257 Trp Glu Gly Ser Thr Phe Ser Gly Gly Tyr Asn Asp Ile Val Ala Gly		465
E--> 1258 470	475	480Asn Leu Ser Trp Pro Arg Ala Ser Asn
1259 Asn Asp Ser Asn Asn Val Tyr		485 490
E--> 1260 495	Asp Leu Trp His Ala Ala Val Asn Ser Arg Gly Glu Phe Phe Ser Ala	
E--> 1261 500	505	510 Asp Ser Pro Asp Gln Leu Val
1262 Ala Ala Phe Gln Asp Ile Leu Asn Arg		515 520
E--> 1263 525	Ile Ser Gly Lys Asp Leu Pro Ala Ser Arg Pro Ala Ile Ser Ser Ser	
E--> 1264 530	535	540 Leu Gln Glu Asp Asp
1265 Thr Gly Asp Lys Leu Thr Arg Phe Ala Tyr Gln	545	550
E--> 1266 555	560Thr Ser Phe Ala Ser Asp Lys Asn Trp Ala Gly Asp Leu Thr	
E--> 1267 Arg Tyr	565	570 575 Ser Leu
1268 Thr Thr Gln Asp Lys Ala Thr Val Gln Thr Asn Leu Trp Ser		580
E--> 1269 585	590 Ala Gln Ser Ile Leu Asp Ala Met Pro Asn Gly Gly	
1270 Ala Gly Arg Lys	595	600 605
1271 Ile Met Met Ala Gly Ser Gly Thr Ser Gly Leu Lys Glu Phe Thr Trp		610
E--> 1272 615	620	Gly Ser Leu Ser Ala Asp Gln Gln Arg Lys
1273 Leu Asn Arg Asp Pro Asp	625	630 635
E--> 1274 640Arg Asn Asp Val Ala Asp Thr Lys Gly Gln Asp Arg Val Ala Phe Leu		
E--> 1275 645	650	655 Arg Gly Asp Arg Arg Lys Glu Asn
1276 Ser Asp Asn Phe Arg Thr Arg Asn		660 665
E--> 1277 670	Ser Ile Leu Gly Asp Ile Ile Asn Ser Ser Pro Ala Thr Val Gly Lys	
E--> 1278 675	680	685 Ala Gln Tyr Leu Thr Tyr
1279 Leu Ala Gln Pro Ile Glu Pro Ser Gly Asn	690	695
E--> 1280 700	Tyr Ser Thr Phe Ala Glu Ala Gln Lys Thr Arg Ala Pro Arg Val	
E--> 1281 Tyr705	710	715 720Val Gly Ala
1282 Asn Asp Gly Met Leu His Gly Phe Asp Thr Asp Gly Asn		725
E--> 1283 730	735 Glu Thr Phe Ala Phe Ile Pro Ser Ala Val Phe Glu Lys	
E--> 1284 Leu His Lys	740	745 750 Leu
1285 Thr Ala Arg Gly Tyr Gln Gly Gly Ala His Gln Phe Tyr Val Asp		755
E--> 1286 760	765	Gly Ser Pro Val Val Ala Asp Ala Phe Phe Gly

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1287	Gly Ala Trp His Thr	770	775	780
1288	Val Leu Ile Gly Ser Leu Arg Ala Gly Gly Lys		Gly Leu Phe Ala Leu	785
E--> 1289	790	795	800Asp Val Thr Asp Pro Ala Asn Ile Lys	
1290	Leu Leu Trp Glu Ile Gly Val		805	810
E--> 1291	815 Asp Gln Glu Pro Asp Leu Gly Tyr Ser	Phe Pro Lys Pro Thr Val Ala		
E--> 1292	820	825	830 Arg Leu His Asn Gly Lys Trp	
1293	Ala Val Val Thr Gly Asn Gly Tyr Ser		835	840
E--> 1294	845 Ser Leu Asn Asp Lys Ala Ala Leu Leu Ile Ile	Asp Leu Glu Thr Gly		
E--> 1295	850	855	860 Ala Ile Thr Arg Lys	
1296	Leu Glu Val Thr Gly Arg Thr Gly Val Pro Asn	865		870
E--> 1297	875 880Gly Leu Ser Ser Leu Arg Leu Ala Asp Asn Asn	Ser Asp Gly		
E--> 1298	Val Ala 885	890	895 Asp Tyr	
1299	Ala Tyr Ala Gly Asp Leu Gln Gly Asn Leu Trp Arg Phe Asp			900
E--> 1300	905 910 Leu Ile Ala Gly Lys Val Asn Gln Asp Asp Pro Phe			
1301	Ser Arg Ala Asn 915	920	925	
1302	Asp Gly Pro Thr Val Ala Ser Ser Phe Arg Val Ser Phe Gly Gly Gln			930
E--> 1303	935 940 Pro Leu Tyr Ser Ala Val Asp Ser Ala Gly			
1304	Ala Ala Gln Ala Ile Thr945	950	955	
E--> 1305	960Ala Ala Pro Ser Leu Val Arg His Pro Thr Arg Lys Gly Tyr Ile Val			
E--> 1306	965 970 Ile Phe Gly Thr Gly Lys Tyr Phe			
1307	Glu Asn Ala Asp Ala Arg Ala Asp	980	985	
E--> 1308	990 Thr Ser Arg Ala Gln Thr Leu Tyr Gly Ile Trp Asp Gln Gln Thr Lys			
E--> 1309	995 1000 Gly Glu Ala Ala Gly Ser			
1310	Thr Pro Arg Leu Thr Arg Gly Asn Leu Gln	1010	1015	
E--> 1311	1020 Gln Gln Thr Leu Asp Leu Gln Ala Asp Ser Thr Phe Ala Ser Thr			
E--> 1312	Ala1025 1030 1035 104Arg Thr Ile			
1313	Arg Ile Gly Ser Gln Asn Pro Val Asn Trp Leu Asn Asn		1045	
E--> 1314	1050 1055 Asp Gly Ser Thr Lys Gln Ser Gly Trp Tyr Leu Asp Phe			
E--> 1315	Met Val Asn 1060 1065 1070 Gly			
1316	Thr Leu Lys Gly Glu Met Leu Ile Glu Asp Met Ile Ala Ile Gly			1075
E--> 1317	1080 1085 Gln Val Val Leu Leu Gln Thr Ile Thr Pro Asn			
1318	Asp Asp Pro Cys Ala 1090 1095 1100			
1319	Asp Gly Ala Ser Asn Trp Thr Tyr Gly Leu Asp Pro Tyr Thr Gly	1105		
E--> 1320	1110 1115 112Arg Thr Arg Phe Thr Val Phe Asp Leu			
1321	Gly Arg Gln Gly Val Val Gly	1125	1130	
E--> 1322	1135 Leu Glu Ile Arg Leu Thr Gly Thr Arg Arg Asn Val Gly Asn Pro			
E--> 1323	1140 1145 1150 Val Pro Ser Arg Lys Ala Trp			
E--> 1324	Glu Ala 1155 1160			

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:32 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:32 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:1
L:33 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:34 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:34 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:35 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:35 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:36 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:36 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:37 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:37 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:38 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:38 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:39 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:39 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:40 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:40 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:41 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:41 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:42 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:42 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:43 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:43 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:44 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:44 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:45 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:45 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:46 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:46 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:47 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:47 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:48 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:48 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:49 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:49 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:50 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:50 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
M:254 Repeated in SeqNo=1
L:50 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
L:50 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1090 Found:70 SEQ:1
L:63 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:63 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:2
L:64 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:65 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:65 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:66 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2

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L:66 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:67 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:67 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
M:254 Repeated in SeqNo=2
L:67 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:67 M:252 E: No. of Seq. differs, <211>LENGTH:Input:277 Found:97 SEQ:2
L:80 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:80 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:3
L:81 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:82 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:82 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:83 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:83 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:84 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:84 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:85 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:85 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:86 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:86 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:87 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:87 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:88 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:88 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:89 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:89 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:90 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:90 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:91 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:91 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:92 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:92 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:93 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:93 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
M:254 Repeated in SeqNo=3
L:93 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:93 M:252 E: No. of Seq. differs, <211>LENGTH:Input:819 Found:99 SEQ:3
L:106 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:106 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:4
L:107 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:108 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:108 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:109 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:109 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:110 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:110 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:111 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:112 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:112 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6

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L:113 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:113 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:114 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:114 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:115 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:115 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:116 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:116 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:117 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:117 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:118 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
 L:119 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 M:254 Repeated in SeqNo=4
 L:119 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:119 M:252 E: No. of Seq. differs, <211>LENGTH:Input:832 Found:112 SEQ:4
 L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
 L:132 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:5
 L:133 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:134 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:134 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:135 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:135 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:136 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:136 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:137 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:137 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:138 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:138 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:139 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5.
 L:149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
 M:254 Repeated in SeqNo=5
 L:149 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
 L:149 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1054 Found:94 SEQ:5
 L:162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
 L:162 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:6
 L:176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
 M:254 Repeated in SeqNo=6
 L:176 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:176 M:252 E: No. of Seq. differs, <211>LENGTH:Input:880 Found:100 SEQ:6
 L:189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
 L:189 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:7
 L:201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
 M:254 Repeated in SeqNo=7
 L:201 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:201 M:252 E: No. of Seq. differs, <211>LENGTH:Input:779 Found:119 SEQ:7
 L:214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
 L:214 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:8

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L:228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
M:254 Repeated in SeqNo=8
L:228 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:228 M:252 E: No. of Seq. differs, <211>LENGTH:Input:848 Found:68 SEQ:8
L:241 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:241 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:9
L:249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
M:254 Repeated in SeqNo=9
L:249 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:249 M:252 E: No. of Seq. differs, <211>LENGTH:Input:533 Found:113 SEQ:9
L:262 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:10
L:271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
M:254 Repeated in SeqNo=10
L:271 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:271 M:252 E: No. of Seq. differs, <211>LENGTH:Input:591 Found:111 SEQ:10
L:284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:284 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:11
L:304 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
M:254 Repeated in SeqNo=11
L:304 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
L:304 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1249 Found:109 SEQ:11
L:317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:317 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:12
M:254 Repeated in SeqNo=12
L:323 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:323 M:252 E: No. of Seq. differs, <211>LENGTH:Input:373 Found:73 SEQ:12
L:336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:336 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:13
L:347 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
M:254 Repeated in SeqNo=13
L:347 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:347 M:252 E: No. of Seq. differs, <211>LENGTH:Input:683 Found:83 SEQ:13
L:360 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:360 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:14
M:254 Repeated in SeqNo=14
L:371 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:371 M:252 E: No. of Seq. differs, <211>LENGTH:Input:672 Found:72 SEQ:14
L:384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:384 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:15
L:411 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
M:254 Repeated in SeqNo=15
L:411 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
L:411 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1676 Found:116 SEQ:15
L:424 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:424 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:16
L:435 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
M:254 Repeated in SeqNo=16
L:435 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
L:436 M:252 E: No. of Seq. differs, <211>LENGTH:Input:721 Found:121 SEQ:16

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/673,605

DATE: 02/27/2002

TIME: 13:33:38

Input Set : A:\Ep.txt

Output Set: N:\CRF3\02272002\I673605.raw

L:449 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
 L:449 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:17
 L:456 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
 M:254 Repeated in SeqNo=17
 L:456 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:456 M:252 E: No. of Seq. differs, <211>LENGTH:Input:452 Found:92 SEQ:17
 L:469 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
 L:469 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:18
 L:476 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
 M:254 Repeated in SeqNo=18
 L:476 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:476 M:252 E: No. of Seq. differs, <211>LENGTH:Input:442 Found:82 SEQ:18
 L:489 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
 L:489 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:19
 L:497 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
 M:254 Repeated in SeqNo=19
 L:497 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:497 M:252 E: No. of Seq. differs, <211>LENGTH:Input:538 Found:118 SEQ:19
 L:510 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
 L:510 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:20
 L:513 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
 M:254 Repeated in SeqNo=20
 L:513 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:513 M:252 E: No. of Seq. differs, <211>LENGTH:Input:218 Found:98 SEQ:20
 L:526 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
 L:526 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:21
 L:536 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
 M:254 Repeated in SeqNo=21
 L:536 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:536 M:252 E: No. of Seq. differs, <211>LENGTH:Input:642 Found:102 SEQ:21
 L:549 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
 L:549 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:22
 L:558 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
 M:254 Repeated in SeqNo=22
 L:558 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:558 M:252 E: No. of Seq. differs, <211>LENGTH:Input:583 Found:103 SEQ:22
 L:571 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
 L:571 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:23
 L:576 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
 M:254 Repeated in SeqNo=23
 L:576 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:576 M:252 E: No. of Seq. differs, <211>LENGTH:Input:360 Found:120 SEQ:23
 L:589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
 L:589 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:24
 L:597 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
 M:254 Repeated in SeqNo=24
 L:597 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:597 M:252 E: No. of Seq. differs, <211>LENGTH:Input:494 Found:74 SEQ:24
 L:620 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26

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L:652 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
 L:693 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:695 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:34
 L:695 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 M:332 Repeated in SeqNo=34
 L:696 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:698 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:699 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:699 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:701 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:707 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:715 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:723 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:730 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:730 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:738 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:746 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:749 M:252 E: No. of Seq. differs, <211>LENGTH:Input:595 Found:328 SEQ:34
 L:758 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:760 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
 L:760 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 M:332 Repeated in SeqNo=35
 L:761 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:763 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:764 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:764 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:766 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:768 M:252 E: No. of Seq. differs, <211>LENGTH:Input:119 Found:66 SEQ:35
 L:777 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:779 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
 L:779 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 M:332 Repeated in SeqNo=36
 L:780 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:782 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:783 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:783 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:785 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:791 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:799 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:804 M:252 E: No. of Seq. differs, <211>LENGTH:Input:295 Found:158 SEQ:36
 L:813 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:815 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:37
 L:815 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 M:332 Repeated in SeqNo=37
 L:816 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:818 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:819 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:819 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:821 M:333 E: Wrong sequence grouping, Amino acids not in groups!

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DATE: 02/27/2002

TIME: 13:33:38

Input Set : A:\Ep.txt

Output Set: N:\CRF3\02272002\I673605.raw

L:827 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:835 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:841 M:252 E: No. of Seq. differs, <211>LENGTH:Input:308 Found:158 SEQ:37
 L:850 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:852 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:38
 L:852 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 M:332 Repeated in SeqNo=38
 L:853 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:855 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:856 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:856 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:858 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:864 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:872 M:252 E: No. of Seq. differs, <211>LENGTH:Input:245 Found:129 SEQ:38
 L:881 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:883 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:39
 L:883 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 M:332 Repeated in SeqNo=39
 L:884 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:886 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:887 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:887 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:889 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:895 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:903 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:911 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:916 M:252 E: No. of Seq. differs, <211>LENGTH:Input:375 Found:213 SEQ:39
 L:927 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:40
 M:332 Repeated in SeqNo=40
 L:931 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:962 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:976 M:252 E: No. of Seq. differs, <211>LENGTH:Input:547 Found:306 SEQ:40
 L:987 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:41
 M:332 Repeated in SeqNo=41
 L:991 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:1022 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:1038 M:252 E: No. of Seq. differs, <211>LENGTH:Input:566 Found:311 SEQ:41
 L:1049 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:42
 M:332 Repeated in SeqNo=42
 L:1053 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:1084 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:1085 M:252 E: No. of Seq. differs, <211>LENGTH:Input:406 Found:231 SEQ:42
 L:1096 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:43
 M:332 Repeated in SeqNo=43
 L:1100 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:1121 M:252 E: No. of Seq. differs, <211>LENGTH:Input:290 Found:158 SEQ:43
 L:1132 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:44
 M:332 Repeated in SeqNo=44
 L:1136 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1

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TIME: 13:33:38

Input Set : A:\Ep.txt

Output Set: N:\CRF3\02272002\I673605.raw

L:1146 M:252 E: No. of Seq. differs, <211>LENGTH:Input:185 Found:85 SEQ:44
L:1157 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:45
M:332 Repeated in SeqNo=45
L:1161 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1180 M:252 E: No. of Seq. differs, <211>LENGTH:Input:274 Found:148 SEQ:45
L:1191 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:46
M:332 Repeated in SeqNo=46
L:1195 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1204 M:252 E: No. of Seq. differs, <211>LENGTH:Input:172 Found:85 SEQ:46
L:1215 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:47
M:332 Repeated in SeqNo=47
L:1219 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1250 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1281 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1312 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1324 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1161 Found:654 SEQ:47
L:1335 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:48
M:332 Repeated in SeqNo=48
L:1339 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1343 M:252 E: No. of Seq. differs, <211>LENGTH:Input:115 Found:66 SEQ:48

<110> Smith, John; Smithgene Inc.

<120> Example of a Sequence Listing

<130> 01-00001

<140> PCT/EP98/00001
<141> 1998-12-31

<150> US 08/999,999
<151> 1997-10-15

<160> 4

<170> PatentIn version 2.0

<210> 1
<211> 389
<212> DNA
<213> Paramecium sp.

<220>
<221> CDS
<222> (279)...(389)

<300>
<301> Doe, Richard
<302> Isolation and Characterization of a Gene Encoding a
Protease from Paramecium sp.
<303> Journal of Genes
<304> 1
<305> 4
<306> 1-7
<307> 1988-06-31
<308> 123456
<309> 1988-06-31

<400> 1
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tgtatgtggca attgctggca gtgccacagg ctttcagcc aggcttaggg tgggttccgc 180
cgcggcgccg cggccctct cgcgtctctc tcgcgcctct ctctcgctc cctctcgctc 240

Appendix 3, page 2

ggacacctgatt aggtgagcag gaggaggggg cagttgc atg Met 1 gtt Val tca Ser atg Met 296
ttc Phe 5 agc Ser .

tgc tct ttc aaa tgg cct gga ttt tgt ttg ttt gtt tgc ttc 344
Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu Phe Val Cys Leu Phe Gln
10 15 20

tgt ccc aaa gtc ctc ccc tgt cac tca tca ctg cag ccg aat ctt 389
Cys Pro Lys Val Leu Pro Cys His Ser Ser Leu Cln Pro Asn Leu
25 30 35

<210>

2

<211>

37

<212>

PRT

<213>

Paramecium sp.

<400> 2
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1 5 10 15

Phe Val Cys Leu Phe Cln Cys Pro Lys Val Leu Pro Cys His Ser Ser
20 25 30

Leu Cln Pro Asn Leu
35

<210>

3

<211>

11

<212>

PRT

<213>

Artificial Sequence

<220>

<221> Designed peptide based on size and polarity to act as a linker between the alpha and beta chains of Protein XYZ.

<400> 3
Met Val Asn Leu Glu Pro Met His Thr Glu Ile
1 5 10

<210> 4

<400> 4

000

[Annex VIII follows]

identifiers and their accompanying information as shown in the following table. The numeric identifier shall be used only in the "Sequence Listing." The order and presentation of the items of information in the "Sequence Listing" shall conform to the arrangement given below. Each item of information shall begin on a new line and shall begin with the numeric identifier enclosed in angle brackets as shown. The submission of those items of information designated with an "M" is mandatory. The submission of those items of information designated with an "O" is optional. Numeric identifiers <110> through <170> shall only be set forth at the beginning of the "Sequence Listing." The following table illustrates the numeric identifiers.

Numeric Identifier	Definition	Comments and Format	Mandatory (M) or Optional (O)
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names and/or Initials	M
<120>	Title of Invention		M
<130>	File Reference	Personal file reference	M, when filed prior to assignment of appl. number
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable
<160>	Number of SEQ ID NOS	Count includes total number of SEQ ID NOS	M
<170>	Software	Name of software used to create the Sequence Listing	O
<210>	SEQ ID NO:#:	Response shall be an integer representing the SEQ ID NO shown	M
<211>	Length	Respond with an integer M expressing the number of bases or amino acid residues	M

<212>	Type	Whether presented sequence molecule is DNA, RNA, or PRT (protein). If a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.	M
<213>	Organism	Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.	M
<220>	Feature	Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<221>	Name/Key	Provide appropriate identifier for feature, preferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence
<222>	Location	Specify location within sequence; where appropriate state number of first and last bases/amino acids	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified

		in feature	
<223>	Other Information	Other relevant information; four lines maximum	base was used in a sequence
			M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<300>	Publication Information	Leave blank after <300>	O
<301>	Authors	Preferably max of ten named authors of publication; specify one name per line; preferable format: Surname, Other Names and/or Initials	O
<302>	Title		O
<303>	Journal		O
<304>	Volume		O
<305>	Issue		O
<306>	Pages		O
<307>	Date	Journal date on which data published; specify as yyyy-mm-dd, MMM-yyyy or Season-yyyy	O
<308>	Database Accession Number	Accession number assigned by database including database name	O
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or MMM-yyyy	O
<310>	Patent Document Number	Document number; for patent-type citations only. Specify as, for example, US 07/999,999	O

<311>	Patent Filing Date	Document filing date, for patent-type citations only; specify as yyyy-mm-dd	O
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-dd	O
<313>	Relevant Residues	FROM (position) TO (position)	O
<400>	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line preceding the actual sequence	AM

5. Section 1.824 is revised to read as follows:

1.824 Form and format for nucleotide and/or amino acid sequence submissions in computer readable form.

(a) The computer readable form required by 1.821(c) shall meet the following specifications:

(1) The computer readable form shall contain a single "Sequence Listing" as either a diskette, series of diskettes, or other permissible media outlined in paragraph (c) of this section.

(2) The "Sequence Listing" in paragraph (a) (1) of this section shall be submitted in American Standard Code for Information Interchange (ASCII) text. No other formats shall be allowed.

(3) The computer readable form may be created by any means, such as word processors, nucleotide/amino acid sequence editors or other custom computer programs; however, it shall conform to all specifications detailed in this section.

(4) File compression is acceptable when using diskette media, so long as the compressed file is in a self-extracting format that will decompress on one of the systems described in paragraph (b) of this section.

(5) Page numbering shall not appear within the computer readable form version of the "Sequence Listing" file.

(6) All computer readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed: the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form, the operating system used, a reference number, and an application serial number and filing date, if known.

(b) Computer readable form submissions must meet these format requirements:

(1) Computer: IBM PC/XT/AT, or compatibles, or Apple Macintosh;

(2) Operating System: MS-DOS, Unix or Macintosh;